

SEQUENCE LISTING

<110> LEE, NANCY M
CHEN, LING C

<120> BIOMARKER PANEL FOR COLORECTAL CANCER

<130> CPMC-01000US1

<140>
<141>

<160> 88

<170> PatentIn Ver. 2.1

<210> 1
<211> 1629
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (74) .. (274)

<400> 1
gcagagcaca caagcttcta ggacaagagc caggaagaaa ccaccggaag gaaccatctc 60

actgtgtgta aac atg act tcc aag ctg gcc gtg gct ctc ttg gca gcc 109
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala
1 5 10

ttc ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt 157
Phe Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser
15 20 25

gct aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc 205
Ala Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe
30 35 40

cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac 253
His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His
45 50 55 60

tgc gcc aac aca gaa att atg taaagctttc tgatggaga gagctctgtc 304
Cys Ala Asn Thr Glu Ile Met
65

tggaccccaa ggaaaactgg gtgcagaggg ttgtggagaa gttttgaag agggctgaga 364

attcagaatt cataaaaaaa ttcattctct gtggtatcca agaatcagtg aagatgccag 424

tgaaacctca agcaaatcta cttcaacact tcatgtattg tgtgggtctg ttgttagggtt 484

gccagatgca atacaagatt cctggtaaa tttgaattc agtaaacaat gaatagttt 544
 tcattgtacc atgaaatatac cagaacatac ttatatgtaa agtattattt atttgaatct 604
 acaaaaaaca acaaataatt tttaaatata aggatttcc tagatattgc acgggagaat 664
 atacaatag caaaatttag gccaagggcc aagagaatat ccgaacttta atttcaggaa 724
 ttgaatgggt ttgctagaat gtgatattg aagcatcaca taaaaatgtat gggacaataa 784
 attttgccat aaagtcaaat ttagctgaa atcctggatt ttttctgtt aaatctggca 844
 accctagtct gctagccagg atccacaagt ccttgttcca ctgtgccttg gtttctcctt 904
 tatttctaag tggaaaaagt attagccacc atcttacctc acagtatgtgt tgtgaggaca 964
 tgtgaaagca cttaagttt tttcatcata acataaatta tttcaagtgt taacttatta 1024
 acctatttat tatttatgtt tttatthaag catcaaataat ttgtgcaaga atttggaaaa 1084
 atagaagatg aatcattgtat tgaatagttt taaagatgtt atagtaaatt tattttattt 1144
 tagatattaa atgatgtttt attagataaa ttcaatcag ggttttaga ttaaacaac 1204
 aaacaattgg gtacccagtt aaattttcat ttcaagataaa caacaataa ttttttagta 1264
 taagtacatt attgttattc tgaaatttaa attgaactaa caatcctagt ttgatactcc 1324
 cagtcttgc attgccagct gtgtggtag tgctgtgtt aattacggaa taatgagtta 1384
 gaactattaa aacagccaaa actccacagt caatattgtt aatttcttgc tggttgaaac 1444
 ttgtttatta tgtacaataa gattttata atattattta aatgactgca ttttaaataa 1504
 caaggcttta tatttttaac tttaagatgt ttttatgtgc tctccaaatt tttttactg 1564
 tttctgattt tatggaaata taaaagtaaa tatgaaacat ttaaaatata atttgttgc 1624
 aaagt 1629

<210> 2
 <211> 3356
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (98)..(1909)

 <400> 2
 gtccaggaac tcctcagcag cgccctccttc agctccacag ccagacgccc tcagacagca 60

aagcctaccc	ccgcggcg	ccctgcccgc	cgctgcg	atg	ctc	gcc	cgc	gcc	ctg	115						
				Met	Leu	Ala	Arg	Ala	Leu							
				1					5							
ctg	ctg	tgc	gcf	ctg	gcf	ctc	agc	cat	aca	gca	aat	cct	tgc	tgt	163	
Leu	Leu	Cys	Ala	Val	Leu	Ala	Leu	Ser	His	Thr	Ala	Asn	Pro	Cys	Cys	
10							15						20			
tcc	cac	cca	tgt	caa	aac	cga	ggt	gta	tgt	atg	agt	gtg	gga	ttt	gac	211
Ser	His	Pro	Cys	Gln	Asn	Arg	Gly	Val	Cys	Met	Ser	Val	Gly	Phe	Asp	
25							30						35			
cag	tat	aag	tgc	gat	tgt	acc	cg	aca	gga	ttc	tat	gga	gaa	aac	tgc	259
Gln	Tyr	Lys	Cys	Asp	Cys	Thr	Arg	Thr	Gly	Phe	Tyr	Gly	Glu	Asn	Cys	
40							45						50			
tca	aca	ccg	gaa	ttt	ttg	aca	aga	ata	aaa	tta	ttt	ctg	aaa	ccc	act	307
Ser	Thr	Pro	Glu	Phe	Leu	Thr	Arg	Ile	Lys	Leu	Phe	Leu	Lys	Pro	Thr	
55							60					65		70		
cca	aac	aca	gtg	cac	tac	ata	ctt	acc	cac	ttc	aag	gga	ttt	tgg	aac	355
Pro	Asn	Thr	Val	His	Tyr	Ile	Leu	Thr	His	Phe	Lys	Gly	Phe	Trp	Asn	
75							80					85				
gtt	gtg	aat	aac	att	ccc	ttc	ctt	cga	aat	gca	att	atg	agt	tat	gtg	403
Val	Val	Asn	Asn	Ile	Pro	Phe	Leu	Arg	Asn	Ala	Ile	Met	Ser	Tyr	Val	
90							95					100				
ttg	aca	tcc	aga	tca	cat	ttg	att	gac	agt	cca	cca	act	tac	aat	gct	451
Leu	Thr	Ser	Arg	Ser	His	Leu	Ile	Asp	Ser	Pro	Pro	Thr	Tyr	Asn	Ala	
105							110					115				
gac	tat	ggc	tac	aaa	agc	tgg	gaa	gcc	ttc	tct	aac	ctc	tcc	tat	tat	499
Asp	Tyr	Gly	Tyr	Lys	Ser	Trp	Glu	Ala	Phe	Ser	Asn	Leu	Ser	Tyr	Tyr	
120							125					130				
act	aga	gcc	ctt	cct	cct	gtg	cct	gat	gat	tgc	ccg	act	ccc	ttg	ggt	547
Thr	Arg	Ala	Leu	Pro	Pro	Val	Pro	Asp	Asp	Cys	Pro	Thr	Pro	Leu	Gly	
135							140					145		150		
gtc	aaa	ggt	aaa	aag	cag	ctt	cct	gat	tca	aat	gag	att	gtg	gaa	aaa	595
Val	Lys	Gly	Lys	Gln	Leu	Pro	Asp	Ser	Asn	Glu	Ile	Val	Glu	Lys		
155							160					165				
ttg	ctt	cta	aga	aga	aag	ttc	atc	cct	gat	ccc	cag	ggc	tca	aac	atg	643
Leu	Leu	Leu	Arg	Arg	Lys	Phe	Ile	Pro	Asp	Pro	Gln	Gly	Ser	Asn	Met	
170							175					180				
atg	ttt	gca	ttc	ttt	gcc	cag	cac	ttc	acg	cat	cag	ttt	ttc	aag	aca	691
Met	Phe	Ala	Phe	Ala	Gln	His	Phe	Thr	His	Gln	Phe	Phe	Lys	Thr		
185							190					195				
gat	cat	aag	cga	ggg	cca	gct	ttc	acc	aac	ggg	ctg	ggc	cat	ggg	gtg	739
Asp	His	Lys	Arg	Gly	Pro	Ala	Phe	Thr	Asn	Gly	Leu	Gly	His	Gly	Val	

200	205	210	
gac tta aat cat att tac ggt gaa act ctg gct aga cag cgt aaa ctg Asp Leu Asn His Ile Tyr Gly Glu Thr Leu Ala Arg Gln Arg Lys Leu 215 220 225 230			787
cgc ctt ttc aag gat gga aaa atg aaa tat cag ata att gat gga gag Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr Gln Ile Ile Asp Gly Glu 235 240 245			835
atg tat cct ccc aca gtc aaa gat act cag gca gag atg atc tac cct Met Tyr Pro Pro Thr Val Lys Asp Thr Gln Ala Glu Met Ile Tyr Pro 250 255 260			883
cct caa gtc cct gag cat cta cg ^g ttt gct gtg ggg cag gag gtc ttt Pro Gln Val Pro Glu His Leu Arg Phe Ala Val Gly Gln Glu Val Phe 265 270 275			931
ggt ctg gtg cct ggt ctg atg atg tat gcc aca atc tgg ctg cg ^g gaa Gly Leu Val Pro Gly Leu Met Met Tyr Ala Thr Ile Trp Leu Arg Glu 280 285 290			979
cac aac aga gta tgc gat gtg ctt aaa cag gag cat cct gaa tgg ggt His Asn Arg Val Cys Asp Val Leu Lys Gln Glu His Pro Glu Trp Gly 295 300 305 310			1027
gat gag cag ttg ttc cag aca agc agg cta ata ctg ata gga gag act Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu Ile Leu Ile Gly Glu Thr 315 320 325			1075
att aag att gtg att gaa gat tat gtg caa cac ttg agt ggc tat cac Ile Lys Ile Val Ile Glu Asp Tyr Val Gln His Leu Ser Gly Tyr His 330 335 340			1123
ttc aaa ctg aaa ttt gac cca gaa cta ctt ttc aac aaa caa ttc cag Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu Phe Asn Lys Gln Phe Gln 345 350 355			1171
tac caa aat cgt att gct gct gaa ttt aac acc ctc tat cac tgg cat Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn Thr Leu Tyr His Trp His 360 365 370			1219
ccc ctt ctg cct gac acc ttt caa att cat gac cag aaa tac aac tat Pro Leu Leu Pro Asp Thr Phe Gln Ile His Asp Gln Lys Tyr Asn Tyr 375 380 385 390			1267
caa cag ttt atc tac aac aac tct ata ttg ctg gaa cat gga att acc Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu Leu Glu His Gly Ile Thr 395 400 405			1315
cag ttt gtt gaa tca ttc acc agg caa att gct ggc agg gtt gct ggt Gln Phe Val Glu Ser Phe Thr Arg Gln Ile Ala Gly Arg Val Ala Gly 410 415 420			1363

ggt agg aat gtt cca ccc gca gta cag aaa gta tca cag gct tcc att Gly Arg Asn Val Pro Pro Ala Val Gln Lys Val Ser Gln Ala Ser Ile 425 430 435	1411
gac cag agc agg cag atg aaa tac cag tct ttt aat gag tac cgc aaa Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser Phe Asn Glu Tyr Arg Lys 440 445 450	1459
cgc ttt atg ctg aag ccc tat gaa tca ttt gaa gaa ctt aca gga gaa Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe Glu Glu Leu Thr Gly Glu 455 460 465 470	1507
aag gaa atg tct gca gag ttg gaa gca ctc tat ggt gac atc gat gct Lys Glu Met Ser Ala Glu Leu Glu Ala Leu Tyr Gly Asp Ile Asp Ala 475 480 485	1555
gtg gag ctg tat cct gcc ctt ctg gta gaa aag cct cgg cca gat gcc Val Glu Leu Tyr Pro Ala Leu Leu Val Glu Lys Pro Arg Pro Asp Ala 490 495 500	1603
atc ttt ggt gaa acc atg gta gaa gtt gga gca cca ttc tcc ttg aaa Ile Phe Gly Glu Thr Met Val Glu Val Gly Ala Pro Phe Ser Leu Lys 505 510 515	1651
gga ctt atg ggt aat gtt ata tgt tct cct gcc tac tgg aag cca agc Gly Leu Met Gly Asn Val Ile Cys Ser Pro Ala Tyr Trp Lys Pro Ser 520 525 530	1699
act ttt ggt gga gaa gtg ggt ttt caa atc atc aac act gcc tca att Thr Phe Gly Gly Glu Val Gly Phe Gln Ile Ile Asn Thr Ala Ser Ile 535 540 545 550	1747
cag tct ctc atc tgc aat aac gtg aag ggc tgt ccc ttt act tca ttc Gln Ser Leu Ile Cys Asn Asn Val Lys Gly Cys Pro Phe Thr Ser Phe 555 560 565	1795
agt gtt cca gat cca gag ctc att aaa aca gtc acc atc aat gca agt Ser Val Pro Asp Pro Glu Leu Ile Lys Thr Val Thr Ile Asn Ala Ser 570 575 580	1843
tct tcc cgc tcc gga cta gat gat atc aat ccc aca gta cta cta aaa Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn Pro Thr Val Leu Leu Lys 585 590 595	1891
gaa cgt tcg act gaa ctg tagaagtcta atgatcatat ttatTTTTT Glu Arg Ser Thr Glu Leu 600	1939
atatgaacca tgtctattaa tttaattatt taataatatt tatattaaac tccttatgtt acttaacatc ttctgtaaca gaagtcagta ctcctgttgc ggagaaaagga gtcataacttg tgaagacttt tatgtcacta ctctaaagat tttgctgttg ctgttaagtt tggaaaacag	1999 2059 2119

ttttattct gtttataaaa ccagagagaa atgagtttg acgtctttt acttgaattt 2179
 caacttatat tataagaacg aaagtaaaga tgtttgaata cttaaacact gtcacaagat 2239
 ggcaaaatgc tgaaagttt tacactgtcg atgttccaa tgcatttcc atgatgcatt 2299
 agaagtaact aatgttgaa attttaagt actttgggtt attttctgt catcaaacaa 2359
 aaacaggtat cagtgcatta ttaaatgaat atttaaatta gacattacca gtaatttcat 2419
 gtctactttt taaaatcagc aatgaaacaa taatttgaaa tttctaaatt cataggtag 2479
 aatcacctgt aaaagcttgt ttgatttctt aaagtttata aacttgtaca tataccaaaa 2539
 agaagctgtc ttggatttaa atctgtaaaa tcagtagaaa ttttactaca attgcttgg 2599
 aaaatatttt ataagtgtatg ttccttttc accaagagta taaaccttt tagtgtgact 2659
 gttaaaactt cctttaaat caaaatgcc aatttattaa ggtggggag ccactgcagt 2719
 gttatcttaa aataagaata ttttggatg atattccaga atttggat atggctggta 2779
 acatgtaaaaa tctatatcag caaaagggtc taccttaaa ataagcaata acaaagaaga 2839
 aaaccaaattt attgttcaaa tttaggttta aacttttgaa gcaaactttt ttttacctt 2899
 gtgcactgca ggcctggta tcagatttg ctatgagggtt aatgaagtac caagctgtgc 2959
 ttgaataatg atatgttttc tcagatttc tggatgtacag tttaatttag cagtcatat 3019
 cacattgcaa aagtagcaat gacctcataa aataacctttt caaaatgctt aaattcattt 3079
 cacacattaa ttttatctca gtcttgaagc caattcagta ggtgcattgg aatcaagcct 3139
 ggctacctgc atgctgtcc ttttcttttc ttcttttagc cattttgcta agagacacag 3199
 tcttcatc acttcgtttc tcctattttg ttttactagt tttaagatca gagttcactt 3259
 tctttggact ctgcctataat tttcttacct gaactttgc aagtttcag gtaaacctca 3319
 gtcaggact gctatttagc tcctcttaag aagatta 3356

<210> 3
 <211> 1750
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (53)..(1132)

<400> 3

cctacaggtg	aaaagccag	cgaccaggc	aggat	ttaag	tttaccta	aa	atg	gaa	58								
							Met	Glu									
									1								
gat	ttt	aac	atg	gag	agt	gac	agc	ttt	gaa	gat	ttc	tgg	aaa	ggt	gaa	106	
Asp		Phe	Asn	Met	Glu	Ser	Asp	Ser	Phe	Glu	Asp	Phe	Trp	Lys	Gly	Glu	
	5						10									15	
gat	ctt	agt	aat	tac	agt	tac	agc	tct	acc	ctg	ccc	cct	ttt	cta	cta		154
Asp	Leu	Ser	Asn	Tyr	Ser	Tyr	Ser	Ser	Thr	Leu	Pro	Pro	Phe	Leu	Leu		
	20						25									30	
gat	gcc	gcc	cca	tgt	gaa	cca	gaa	tcc	ctg	gaa	atc	aac	aag	tat	ttt		202
Asp	Ala	Ala	Pro	Cys	Glu	Pro	Glu	Ser	Leu	Glu	Ile	Asn	Lys	Tyr	Phe		
	35					40				45						50	
gtg	gtc	att	atc	tat	gcc	ctg	gta	ttc	ctg	ctg	agc	ctg	ctg	gga	aac		250
Val	Val	Ile	Ile	Tyr	Ala	Leu	Val	Phe	Leu	Leu	Ser	Leu	Leu	Gly	Asn		
							55		60							65	
tcc	ctc	gtg	atg	ctg	gtc	atc	tta	tac	agc	agg	gtc	ggc	cgc	tcc	gtc		298
Ser	Leu	Val	Met	Leu	Val	Ile	Leu	Tyr	Ser	Arg	Val	Gly	Arg	Ser	Val		
	70					75				80							
act	gat	gtc	tac	ctg	ctg	aac	cta	gcc	ttg	gcc	gac	cta	ctc	ttt	gcc		346
Thr	Asp	Val	Tyr	Leu	Leu	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Phe	Ala		
	85					90					95						
ctg	acc	ttg	ccc	atc	tgg	gcc	gcc	tcc	aag	gtg	aat	ggc	tgg	att	ttt		394
Leu	Thr	Leu	Pro	Ile	Trp	Ala	Ala	Ser	Lys	Val	Asn	Gly	Trp	Ile	Phe		
	100					105				110							
ggc	aca	ttc	ctg	tgc	aag	gtg	gtc	tca	ctc	ctg	aag	gaa	gtc	aac	ttc		442
Gly	Thr	Phe	Leu	Cys	Lys	Val	Val	Ser	Leu	Leu	Lys	Glu	Val	Asn	Phe		
	115					120				125						130	
tat	agt	ggc	atc	ctg	cta	ctg	gcc	tgc	atc	agt	gtg	gac	cgt	tac	ctg		490
Tyr	Ser	Gly	Ile	Leu	Leu	Ala	Cys	Ile	Ser	Val	Asp	Arg	Tyr	Leu			
						135			140				145				
gcc	att	gtc	cat	gcc	aca	cgc	aca	ctg	acc	cag	aag	cgc	tac	ttg	gtc		538
Ala	Ile	Val	His	Ala	Thr	Arg	Thr	Leu	Thr	Gln	Lys	Arg	Tyr	Leu	Val		
						150			155				160				
aaa	ttc	ata	tgt	ctc	agc	atc	tgg	ggt	ctg	tcc	ttg	ctc	ctg	gcc	ctg		586
Lys	Phe	Ile	Cys	Leu	Ser	Ile	Trp	Gly	Leu	Ser	Leu	Leu	Leu	Ala	Leu		
						165			170				175				
cct	gtc	tta	ctt	ttc	cga	agg	acc	gtc	tac	tca	tcc	aat	gtt	agc	cca		634
Pro	Val	Leu	Leu	Phe	Arg	Arg	Thr	Val	Tyr	Ser	Ser	Asn	Val	Ser	Pro		
						180			185				190				
gcc	tgc	tat	gag	gac	atg	ggc	aac	aat	aca	gca	aac	tgg	cgg	atg	ctg		682
Ala	Cys	Tyr	Glu	Asp	Met	Gly	Asn	Asn	Thr	Ala	Asn	Trp	Arg	Met	Leu		

195	200	205	210	
tta cggtatcctgccc cagttccgttggccatcgtgtccatgcgtatc Leu Arg Ile Leu Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile	215	220	225	730
atgctgttcgtacggatttcaccatgtcgatcgatgtttaaaggcccac Met Leu Phe Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His	230	235	240	778
atggggcagaaacccgggccatgcgggtcatctttgtctgtctctc Met Gly Gln Lys His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu	245	250	255	826
atcttcctgttgc tggccatc tac aac ctgtgtccatgtgtgc Ile Phe Leu Leu Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp	260	265	270	874
accctc atgaggacc caggtgatc cag gag acctgtgagcgcc Thr Leu Met Arg Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn	275	280	285	922
cacatcgacccg gctctgatgccaccgatattctggcatcc His Ile Asp Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His	295	300	305	970
agctgcctcaacccatc tac gat gccatttttttttttttttttt Ser Cys Leu Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg	310	315	320	1018
catgga ctc ctc aag att cta gct ata cat ggc ttgatc His Gly Leu Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp	325	330	335	1066
tccctgtccc aaa gac agc agg ccttccatttttttttttttttt Ser Leu Pro Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly	340	345	350	1114
cacacttccactactctcta taagacacctcc tgccttaagtgc His Thr Ser Thr Thr Leu	355	360		1162
gggttcctcc cttctttca cagtcacattccaaggctca tgccactgg ttcttcttgg				1222
tctcagtgtc aatgcagccc ccattgtggt cacaggaagc agaggaggcc acgttcttac				1282
tagttccct tgcattggttt agaaaagcttg ccctggtgcc tcaccccttg ccataattac				1342
tatgtcattt gctggagctc tgcccatcct gccccctgagc ccatggcact ctatgttcta				1402
agaagtaaaa atctacactc cagttagaca gctctgcata ctcatttagga tggcttagtat				1462
aaaaaqaaaaq aaaatcagqc tggccaaacgg gatgaaaccc tgtctctact aaaaatacaa				1522

aaaaaaa aaaaattagc cgggcgtggt ggtgagtgcc tgtaatcaca gctacttggg 1582
aggctgagat gggagaatca cttgaacccg ggagggcagag gttgcagtga gccgagattg 1642
tgccccctgca ctccagcctg agcgacagtg agactctgtc tcagtcctat aagatgtaga 1702
ggagaaaactg gaactctcga gcgttgcctgg gggggattgt aaaatggt 1750

<210> 4
<211> 597
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(597)

<400> 4
atg ccc cta ggt ctc ctg tgg ctg ggc cta gcc ctg ttg ggg gct ctg 48
Met Pro Leu Gly Leu Leu Trp Leu Gly Leu Ala Leu Leu Gly Ala Leu
1 5 10 15

cat gcc cag gcc cag gac tcc acc tca gac ctg atc cca gcc cca cct 96
His Ala Gln Ala Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro
20 25 30

ctg agc aag gtc cct ctg cag cag aac ttc cag gac aac caa ttc cag 144
Leu Ser Lys Val Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe Gln
35 40 45

ggg aag tgg tat gtg gta ggc ctg gca ggg aat gca att ctc aga gaa 192
Gly Lys Trp Tyr Val Val Gly Leu Ala Gly Asn Ala Ile Leu Arg Glu
50 55 60

gac aaa gac ccg caa aag atg tat gcc acc atc tat gag ctg aaa gaa 240
Asp Lys Asp Pro Gln Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu
65 70 75 80

gac aag agc tac aat gtc acc tcc gtc ctg ttt agg aaa aag aag tgt 288
Asp Lys Ser Tyr Asn Val Thr Ser Val Leu Phe Arg Lys Lys Lys Cys
85 90 95

gac tac tgg atc agg act ttt gtt cca ggt tgc cag ccc ggc gag ttc 336
Asp Tyr Trp Ile Arg Thr Phe Val Pro Gly Cys Gln Pro Gly Glu Phe
100 105 110

acg ctg ggc aac att aag agt tac cct gga tta acg agt tac ctc gtc 384
Thr Leu Gly Asn Ile Lys Ser Tyr Pro Gly Leu Thr Ser Tyr Leu Val
115 120 125

cga gtg gtg agc acc aac tac aac cag cat gct atg gtg ttc ttc aag 432
Arg Val Val Ser Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys

130	135	140	
aaa gtt tct caa aac agg gag tac ttc aag atc acc ctc tac ggg aga Lys Val Ser Gln Asn Arg Glu Tyr Phe Lys Ile Thr Leu Tyr Gly Arg	145 150	155	480
acc aag gag ctg act tcg gaa cta aag gag aac ttc atc cgc ttc tcc Thr Lys Glu Leu Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser	165	170	528
aaa tat ctg ggc ctc cct gaa aac cac atc gtc ttc cct gtc cca atc Lys Tyr Leu Gly Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile	180	185	576
gac cag tgt atc gac ggc tga Asp Gln Cys Ile Asp Gly	195		597

<210> 5
<211> 369
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(369)

atg aag ctt ctc acg ggc ctg gtt ttc tgc tcc ttg gtc ctg ggt gtc Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val	1 5	10	48
agc agc cga agc ttc ttt tcg ttc ctt ggc gag gct ttt gat ggg gct Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala	20	25	96
cg ^g gac atg tgg aga gcc tac tct gac atg aga gaa gcc aat tac atc Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile	35	40	144
ggc tca gac aaa tac ttc cat gct cg ^g ggg aac tat gat gct gcc aaa Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys	50	55	192
agg gga cct gg ^g ggt gtc tgg gct gca gaa gc ^g atc agc gat gcc aga Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg	65 70	75	240
gag aat atc cag aga ttc ttt ggc cat ggt gc ^g gag gac tcg ctg gct Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala	85	90	288
		95	

gat cag gct gcc aat gaa tgg ggc agg agt ggc aaa gac ccc aat cac	336
Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His	
100 105 110	
 ttc cga cct gct ggc ctg cct gag aaa tac tga	369
Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr	
115 120	
 <210> 6	
<211> 3939	
<212> DNA	
<213> Homo sapiens	
 <220>	
<221> CDS	
<222> (106)..(1767)	
 <400> 6	
cctgggtcct ctcggcgcca gagccgctct ccgcattccca ggacagcggt gcggccctcg	60
gccggggcgc ccactccgca gcagccagcg agccagctgc cccgt atg acc gcg ccg	117
Met Thr Ala Pro	
1	
 ggc gcc gcc ggg cgc tgc cct ccc acg aca tgg ctg ggc tcc ctg ctg	165
Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu Gly Ser Leu Leu	
5 10 15 20	
 ttg ttg gtc tgt ctc ctg gcg agc agg agt atc acc gag gag gtg tcg	213
Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr Glu Glu Val Ser	
25 30 35	
 gag tac tgt agc cac atg att ggg agt gga cac ctg cag tct ctg cag	261
Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu Gln Ser Leu Gln	
40 45 50	
 cgg ctg att gac agt cag atg gag acc tcg tgc caa att aca ttt gag	309
Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln Ile Thr Phe Glu	
55 60 65	
 ttt gta gac cag gaa cag ttg aaa gat cca gtg tgc tac ctt aag aag	357
Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys Tyr Leu Lys Lys	
70 75 80	
 gca ttt ctc ctg gta caa gac ata atg gag gac acc atg cgc ttc aga	405
Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr Met Arg Phe Arg	
85 90 95 100	
 gat aac acc gcc aat ccc atc gcc att gtg cag ctg cag gaa ctc tct	453
Asp Asn Thr Ala Asn Pro Ile Ala Ile Val Gln Leu Gln Glu Leu Ser	
105 110 115	

ttg agg ctg aag agc tgc ttc acc aag gat tat gaa gag cat gac aag	501
Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu Glu His Asp Lys	
120 125 130	
gcc tgc gtc cga act ttc tat gag aca cct ctc cag ttg ctg gag aag	549
Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln Leu Leu Glu Lys	
135 140 145	
gtc aag aat gtc ttt aat gaa aca aag aat ctc ctt gac aag gac tgg	597
Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu Asp Lys Asp Trp	
150 155 160	
aat att ttc agc aag aac tgc aac aac agc ttt gct gaa tgc tcc agc	645
Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala Glu Cys Ser Ser	
165 170 175 180	
caa gat gtg gtg acc aag cct gat tgc aac tgc ctg tac ccc aaa gcc	693
Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu Tyr Pro Lys Ala	
185 190 195	
atc cct agc agt gac ccg gcc tct gtc tcc cct cat cag ccc ctc gcc	741
Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His Gln Pro Leu Ala	
200 205 210	
ccc tcc atg gcc cct gtg gct ggc ttg acc tgg gag gac tct gag gga	789
Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu Asp Ser Glu Gly	
215 220 225	
act gag ggc agc tcc ctc ttg cct ggt gag cag ccc ctg cac aca gtg	837
Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro Leu His Thr Val	
230 235 240	
gat cca ggc agt gcc aag cag cgg cca ccc agg agc acc tgc cag agc	885
Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser Thr Cys Gln Ser	
245 250 255 260	
ttt gag ccg cca gag acc cca gtt gtc aag gac agc acc atc ggt ggc	933
Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser Thr Ile Gly Gly	
265 270 275	
tca cca cag cct cgc ccc tct gtc ggg gcc ttc aac ccc ggg atg gag	981
Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn Pro Gly Met Glu	
280 285 290	
gat att ctt gac tct gca atg ggc act aat tgg gtc cca gaa gaa gcc	1029
Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val Pro Glu Glu Ala	
295 300 305	
tct gga gag gcc agt gag att ccc gta ccc caa ggg aca gag ctt tcc	1077
Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly Thr Glu Leu Ser	
310 315 320	
ccc tcc agg cca gga ggg ggc agc atg cag aca gag ccc gcc aga ccc	1125
Pro Ser Arg Pro Gly Gly Ser Met Gln Thr Glu Pro Ala Arg Pro	

325	330	335	340	
agc aac ttc ctc tca gca tct tct cca ctc cct gca tca gca aag ggc Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala Ser Ala Lys Gly				1173
345	350		355	
caa cag ccg gca gat gta act gct aca gcc ttg ccc agg gtg ggc ccc Gln Gln Pro Ala Asp Val Thr Ala Thr Ala Leu Pro Arg Val Gly Pro				1221
360	365		370	
gtg atg ccc act ggc cag gac tgg aat cac acc ccc cag aag aca gac Val Met Pro Thr Gly Gln Asp Trp Asn His Thr Pro Gln Lys Thr Asp				1269
375	380		385	
cat cca tct gcc ctg ctc aga gac ccc ccg gag cca ggc tct ccc agg His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro Gly Ser Pro Arg				1317
390	395		400	
atc tca tca ctg cgc ccc cag gcc ctc agc aac ccc tcc acc ctc tct Ile Ser Ser Leu Arg Pro Gln Ala Leu Ser Asn Pro Ser Thr Leu Ser				1365
405	410		415	420
gct cag cca cag ctt tcc aga agc cac tcc tcg ggc agc gtg ctg ccc Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly Ser Val Leu Pro				1413
425	430		435	
ctt ggg gag ctg gag ggc agg agg agc acc agg gat cgg acg agc ccc Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp Arg Thr Ser Pro				1461
440	445		450	
gca gag cca gaa gca gca cca gca agt gaa ggg gca gcc agg ccc ctg Ala Glu Pro Glu Ala Ala Pro Ala Ser Glu Gly Ala Ala Arg Pro Leu				1509
455	460		465	
ccc cgt ttt aac tcc gtt cct ttg act gac aca ggc cat gag agg cag Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly His Glu Arg Gln				1557
470	475		480	
tcc gag gga tcc tcc agc ccg cag ctc cag gag tct gtc ttc cac ctg Ser Glu Gly Ser Ser Pro Gln Leu Gln Glu Ser Val Phe His Leu				1605
485	490		495	500
ctg gtg ccc agt gtc atc ctg gtc ttg ctg gct gtc gga ggc ctc ttg Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val Gly Gly Leu Leu				1653
505	510		515	
ttc tac agg tgg agg cgg cgg agc cat caa gag cct cag aga gcg gat Phe Tyr Arg Trp Arg Arg Ser His Gln Glu Pro Gln Arg Ala Asp				1701
520	525		530	
tct ccc ttg gag caa cca gag ggc agc ccc ctg act cag gat gac aga Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg				1749
535	540		545	

cag gtg gaa ctg cca gtg tagagggaat tctaagctgg acgcacagaa 1797
 Gln Val Glu Leu Pro Val
 550

cagtctttc gtgggaggag acattatggg gcgtccacca ccaccctcc ctggccatcc 1857
 tccttggaaatg tggtctgccc tccaccagag ctctgcctg ccaggactgg accagagcag 1917
 ccaggctggg gccccctgt ctcaaccgc agacccttga ctgaatgaga gaggccagag 1977
 gatgctcccc atgctgccac tatttatgt gagcccttga ggctccatg tgcttgagga 2037
 aggctggtga gcccggtca ggacccttt ccctcagggg ctgcagcctc ctctcactcc 2097
 ctccatgcc ggaaccagg ccagggaccc accggcctgt ggtttgggg aaagcagggt 2157
 gcacgctgag gagtgaaca accctgcacc cagagggcct gcctggtgc aaggtatccc 2217
 agcctggaca ggcattggacc tgtctccaga cagaggagcc tgaagttcgt gggggggac 2277
 agcctcgcc tgatttcccg taaaggtgt cagcctgaga gacgggaaga ggaggcctct 2337
 gcacctgctg gtctgcactg acagcctgaa gggctcacac ctcggctca cctaagtccc 2397
 tgtgctgggtt gccaggcca gaggggaggc cagccctgcc ctcaggacct gcctgacctg 2457
 ccagtgtgc caagaggggg atcaagca ggccttgcc ctcctccctt ccagcacctg 2517
 ccagagcttc tccagcaggg caagcagagg ctccctcat gaaggaagcc attgcactgt 2577
 gaacactgta ctcgcctgct gaacagcctc ccccggtcca tccatgagcc agcatccgtc 2637
 cgtccctccac tctccagcct ctcctcagcc tcctgcactg agctggcctc accagtcgac 2697
 tgagggagcc ctcagccct gaccttctcc tgacctggcc tttgactccc cggagtggag 2757
 tgggggtggga gAACCTCCTG ggccgcccagc cagagccgct cttaggctg tgttctcgc 2817
 ccaggtttct gcatcttcca cttagacatt cccaaagaggg aaggacttag tgggagagag 2877
 caagggaggg gagggcacag acagagagcc tacagggcga gctctgactg aagatgggccc 2937
 ttggaaatat aggtatgcac ctgagggttgg gggagggtct gcactccaa accccagcgc 2997
 agtgtccctt ccctgctgcc gacaggaacc tggggctgag caggttatcc ctgtcaggag 3057
 ccctggactg ggctgcatac cagccccacc tgcattggat ccagctccca tccacttctc 3117
 acccttctt ctcctgacc ttggtcagca gtgtacccctt ccaactctca cccacccct 3177
 ctaccatcac ctctaacccag gcaagccagg gtgggagagc aatcaggaga gccaggcctc 3237
 agcttccaaat gcctggaggg ctcctttt gtggccagcc tgggtgctg gctctgaggc 3297

ctaggcaacg agcgacaggg ctgccagttg cccctgggtt ccttgcgtc gctgtgtgcc 3357
tcctctcctg ccgccccttg tcctccgcta agagaccctg ccctacctgg ccgctgggcc 3417
ccgtgacttt cccttcctgc ccaggaaagt gagggtcggc tggccccacc ttccctgtcc 3477
tgtatgccgac agcttaggga agggcactga acttgcataat ggggcttagc cttctagtca 3537
cagcctctat atttgatgct agaaaaacaca tatttttaaa tggaaagaaaa ataaaaaaggc 3597
attccccctt catcccccta ccttaaacat ataatatttt aaaggtaaaa aaagcaatcc 3657
aacccactgc agaagctctt tttgagcact tgggtggcatc agagcaggag gagccccaga 3717
gccacctctg gtgtccccca ggctacctgc tcaggaaccc cttctgttct ctgagaactc 3777
aacagaggac attggctcac gcactgtgag attttgtttt tatacttgca actggtgaat 3837
tattttttat aaagtcattt aaatatctat ttaaaaagata ggaagctgct tatatattta 3897
ataataaaaq aagtgcacaaa qctggccgttg acgttagctcg ag 3939

```

<210> 7
<211> 1024
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(321)

<400> 7
atg gcc cgc gct gct ctc tcc gcc gcc ccc agc aat ccc cgg ctc ctg      48
Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
 1           5               10            15

cga gtg gca ctg ctg ctc ctg gta gcc gct ggc cgg cgc gca      96
Arg Val Ala Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala
 20          25            30

gca gga gcg tcc gtg gcc act gaa ctg cgc tgc cag tgc ttg cag acc      144
Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
 35          40            45

ctg cag gga att cac ccc aag aac atc caa agt gtg aac gtg aag tcc      192
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
 50          55            60

ccc gga ccc cac tgc gcc caa acc gaa gtc ata gcc aca ctc aag aat      240
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
 65          70            75            80

```

ggg cgg aaa gct tgc ctc aat cct gca tcc ccc ata gtt aag aaa atc 288
Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
85 90 95

atc gaa aag atg ctg aac agt gac aaa tcc aac tgaccagaag ggaggaggaa 341
Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
100 105

gctcactgggt ggctgttcct gaaggaggcc ctgcccttat aggaacagaa gaggaagag 401
agacacagct gcagaggcca cctggattgt gcctaatgtg tttgagcatc gcttaggaga 461
agtcttctat ttatttattt attcatttagt tttgaagatt ctatgttaat attttaggtg 521
taaaataatt aagggtatga ttaactctac ctgcacactg tcctattata ttcattcttt 581
ttgaaatgtc aaccccaagt tagttcaatc tggattcata ttaatttga aggtagaatg 641
ttttcaaatg ttctccagtc attatgttaa tatttctgag gagcctgcaa catgccagcc 701
actgtgatag aggctggcg 8 atccaagcaa atggccaaatg agatcattgt gaaggcaggg 761
aatgtatgt gcacatctgt tttgttaactg ttttagatgaa tgtcagttgt tatttattga 821
aatgattca cagtgtgtgg tcaacatttc tcatgttcaa actttaagaa ctaaaatgtt 881
ctaaatatcc cttggacatt ttatgtcttt cttgttaaggc atactgcctt gtttaatgg 941
agttttacag tgtttctggc tttagaaca 9 ggggcttaat tattgtatgtt ttcatagaga 1001
atataaaaat aaagcactta tag 1024

<210> 8
<211> 1064
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (78) .. (395)

<220>
<221> modified_base
<222> (27)
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (766)
<223> a, c, t, g, other or unknown

<400> 8

cacagccggg tcgcaggcac ctccccngcc agctctcccg cattctgcac agtttccga 60
 cgcgtctgct gagcccc atg gcc cac gcc acg ctc tcc gcc gcc ccc agc 110
 Met Ala His Ala Thr Leu Ser Ala Ala Pro Ser
 1 5 10

 aat ccc cgg ctc ctg cgg gtg gcg ctg ctg ctc ctg ctg ctg gtg ggc 158
 Asn Pro Arg Leu Leu Arg Val Ala Leu Leu Leu Leu Leu Val Gly
 15 20 25

 agc cgg cgc gca gca gga gcg tcc gtg gtc act gaa ctg cgc tgc cag 206
 Ser Arg Arg Ala Ala Gly Ala Ser Val Val Thr Glu Leu Arg Cys Gln
 30 35 40

 tgc ttg cag aca ctg cag gga att cac ctc aag aac atc caa agt gtg 254
 Cys Leu Gln Thr Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val
 45 50 55

 aat gta agg tcc ccc gga ccc cac tgc gcc caa acc gaa gtc ata gcc 302
 Asn Val Arg Ser Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala
 60 65 70 75

 aca ctc aag aat ggg aag aaa gct tgt ctc aac ccc gca tcc ccc atg 350
 Thr Leu Lys Asn Gly Lys Ala Cys Leu Asn Pro Ala Ser Pro Met
 80 85 90

 gtt cag aaa atc atc gaa aag ata ctg aac aag ggg agc acc aac 395
 Val Gln Lys Ile Ile Glu Lys Ile Leu Asn Lys Gly Ser Thr Asn
 95 100 105

 tgacaggaga gaagtaagaa gcttatcagc gtatcattga cacttcctgc agggtgttcc 455
 ctgcccttac cagagctgaa aatgaaaaag agaacagcag ctttcttaggg acagctggaa 515
 agggacttaa tgtgtttgac tatttcttac gagggttcta cttatattatg tatttattt 575
 tgaaaagctt tattttataa ttttacatgc tgttatttaa agatgtgagt gtgtttcatc 635
 aaacatagct cagtcctgat tatttaattt gaatatgtatg ggttttaaat gtgtcattaa 695
 actaatattt agtggggagac cataatgtgt cagccacctt gataaatgac aggggtgggaa 755
 actggagggt ngggggattt aatgcaagc aatttagtgga tcactgttag ggtaagggaa 815
 tgtatgtaca catctatattt ttatactttt ttttttaaaa aagaatgtca gttgttattt 875
 attcaaatta tctcacatta tgtgttcaac atttttatgc tgaagttcc cttagacatt 935
 ttatgtcttg cttgttagggc ataatgcctt gtttaatgtc cattctgcag cgtttctt 995
 tcccttggaa aagagaattt atcattactg ttacatttgc acaaatgaca tgataataaa 1055
 agttttatg 1064

```

<210> 9
<211> 1469
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (102)..(1001)

<400> 9
agcagcagga ggaggcagag cacagcatcg tcgggaccag actcgctca ggccagttgc 60
agccttctca gccaaacgcc gaccaaggaa aactcaactac c atg aga att gca gtg 116
                                         Met Arg Ile Ala Val
                                         1           5

att tgc ttt tgc ctc cta ggc atc acc tgt gcc ata cca gtt aaa cag 164
Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala Ile Pro Val Lys Gln
      10          15          20

gct gat tct gga agt tct gag gaa aag cag ctt tac aac aaa tac cca 212
Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu Tyr Asn Lys Tyr Pro
      25          30          35

gat gct gtg gcc aca tgg cta aac cct gac cca tct cag aag cag aat 260
Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro Ser Gln Lys Gln Asn
      40          45          50

ctc cta gcc cca cag acc ctt cca agt aag tcc aac gaa agc cat gac 308
Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser Asn Glu Ser His Asp
      55          60          65

cac atg gat gat atg gat gat gaa gat gat gac cat gtg gac agc 356
His Met Asp Asp Met Asp Asp Glu Asp Asp Asp His Val Asp Ser
      70          75          80          85

cag gac tcc att gac tcg aac gac tct gat gat gta gat gac act gat 404
Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp Asp Thr Asp
      90          95          100

gat tct cac cag tct gat gag tct cac cat tct gat gaa tct gat gaa 452
Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu Ser Asp Glu
      105         110         115

ctg gtc act gat ttt ccc acg gac ctg cca gca acc gaa gtt ttc act 500
Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu Val Phe Thr
      120         125         130

cca gtt gtc ccc aca gta gac aca tat gat ggc cga ggt gat agt gtg 548
Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Arg Gly Asp Ser Val
      135         140         145

```

gtt tat gga ctg agg tca aaa tct aag aag ttt cgc aga cct gac atc	596
Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg Pro Asp Ile	
150 155 160 165	
cag tac cct gat gct aca gac gag gac atc acc tca cac atg gaa agc	644
Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His Met Glu Ser	
170 175 180	
gag gag ttg aat ggt gca tac aag gcc atc ccc gtt gcc cag gac ctg	692
Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala Gln Asp Leu	
185 190 195	
aac gcg cct tct gat tgg gac agc cgt ggg aag gac agt tat gaa acg	740
Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser Tyr Glu Thr	
200 205 210	
agt cag ctg gat gac cag agt gct gaa acc cac agc cac aag cag tcc	788
Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His Ser His Lys Gln Ser	
215 220 225	
aga tta tat aag cgg aaa gcc aat gat gag agc aat gag cat tcc gat	836
Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu His Ser Asp	
230 235 240 245	
gtg att gat agt cag gaa ctt tcc aaa gtc agc cgt gaa ttc cac agc	884
Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu Phe His Ser	
250 255 260	
cat gaa ttt cac agc cat gaa gat atg ctg gtt gta gac ccc aaa agt	932
His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp Pro Lys Ser	
265 270 275	
aag gaa gaa gat aaa cac ctg aaa ttt cgt att tct cat gaa tta gat	980
Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His Glu Leu Asp	
280 285 290	
agt gca tct tct gag gtc aat taaaaggaga aaaaatacaa tttctcactt	1031
Ser Ala Ser Ser Glu Val Asn	
295 300	
 tgcattagt caaaagaaaa aatgcttat agcaaatga aagagaacat gaaatgcttc 1091	
 tttctcagtt tatttgttga atgtgtatct atttgagtct ggaaataact aatgtgtttg 1151	
 ataattagtt tagtttgtgg cttcatggaa actccctgta aactaaaagc ttcagggtta 1211	
 tgtctatgtt cattctatag aagaaatgca aactatcact gtattttaat atttgttatt 1271	
 ctctcatgaa tagaaaattta tgtagaagca aacaaaatac ttttacccac taaaaaagag 1331	
 aatataacat ttatgtcac tataatctt tgtttttaa gtttagtgtat attttgttgc 1391	
 gattatctt ttgtgggttg aataaatctt ttatcttgcg tgtaataaga aaaaaaaaaa 1451	

aaaaacaaaa aaaaaaaa	1469
<210> 10	
<211> 1256	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (145)..(1029)	
<400> 10	
gcagtagcag cgaggcagcag agtccgcacg ctccggcgag gggcagaaga ggcgcaggga	60
gcgcggggca gcagaagcga gagccgagcg cggaccac caggaccac agccctcccc	120
agctgccca agagagcccc agcc atg gaa cac cag ctc ctg tgc tgc gaa	171
Met Glu His Gln Leu Leu Cys Cys Glu	
1	5
gtg gaa acc atc cgc cgc gcg tac ccc gat gcc aac ctc ctc aac gac	219
Val Glu Thr Ile Arg Arg Ala Tyr Pro Asp Ala Asn Leu Leu Asn Asp	
10	15
20	25
cggtgtctgcgggccatgctgaaggcggagggacc tgc gcg ccc tcg	267
Arg Val Leu Arg Ala Met Leu Lys Ala Glu Glu Thr Cys Ala Pro Ser	
30	35
40	
gtgtcc tac ttc aaa tgt gtg cag aag gag gtc ctg ccgtccatgcgg	315
Val Ser Tyr Phe Lys Cys Val Gln Lys Glu Val Leu Pro Ser Met Arg	
45	50
55	
aag atc gtc gcc acc tgg atg ctg gag gtc tgc gag gaa cag aag tgc	363
Lys Ile Val Ala Thr Trp Met Leu Glu Val Cys Glu Glu Gln Lys Cys	
60	65
70	
gag gag gag gtc ttc ccgtctg gccc atg aac tac ctg gac cgc ttctg	411
Glu Glu Val Phe Pro Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu	
75	80
85	
tcgtctggccgtaaa aag agc cgc ctgcag ctgcctggggccact	459
Ser Leu Glu Pro Val Lys Lys Ser Arg Leu Gln Leu Leu Gly Ala Thr	
90	95
100	105
tgc atg ttc gtg gcc tct aag atg aag gag acc atc ccc ctg acg gcc	507
Cys Met Phe Val Ala Ser Lys Met Lys Glu Thr Ile Pro Leu Thr Ala	
110	115
120	
gag aag ctg tgc atc tac acc gac ggc tcc atc cgg ccc gag gag ctg	555
Glu Lys Leu Cys Ile Tyr Thr Asp Gly Ser Ile Arg Pro Glu Glu Leu	
125	130
135	

ctg caa atg gag ctg ctc ctg gtg aac aag ctc aag tgg aac ctg gcc	603
Leu Gln Met Glu Leu Leu Leu Val Asn Lys Leu Lys Trp Asn Leu Ala	
140 145 150	
gca atg acc ccg cac gat ttc att gaa cac ttc ctc tcc aaa atg cca	651
Ala Met Thr Pro His Asp Phe Ile Glu His Phe Leu Ser Lys Met Pro	
155 160 165	
gag gcg gag gag aac aaa cag atc atc cgc aaa cac gcg cag acc ttc	699
Glu Ala Glu Glu Asn Lys Gln Ile Ile Arg Lys His Ala Gln Thr Phe	
170 175 180 185	
gtt gcc tct tgt gcc aca gat gtg aag ttc att tcc aat ccg ccc tcc	747
Val Ala Ser Cys Ala Thr Asp Val Lys Phe Ile Ser Asn Pro Pro Ser	
190 195 200	
atg gtg gca gcg ggg agc gtg gtg gca gtg caa ggc ctg aac ctg	795
Met Val Ala Ala Gly Ser Val Val Ala Ala Val Gln Gly Leu Asn Leu	
205 210 215	
agg agc ccc aac aac ttc ctg tcc tac tac cgc ctc aca cgc ttc ctc	843
Arg Ser Pro Asn Asn Phe Leu Ser Tyr Tyr Arg Leu Thr Arg Phe Leu	
220 225 230	
tcc aga gtg atc aag tgt gac cca gac tgc ctc cgg gcc tgc cag gag	891
Ser Arg Val Ile Lys Cys Asp Pro Asp Cys Leu Arg Ala Cys Gln Glu	
235 240 245	
cag atc gaa gcc ctg ctg gag tca agc ctg cgc cag gcc cag cag aac	939
Gln Ile Glu Ala Leu Leu Glu Ser Ser Leu Arg Gln Ala Gln Gln Asn	
250 255 260 265	
atg gac ccc aag gcc gag gag gag gaa gag gag gag gag gtg	987
Met Asp Pro Lys Ala Ala Glu Glu Glu Glu Glu Glu Glu Val	
270 275 280	
gac ctg gct tgc aca ccc acc gac gtg cgg gac gtg gac atc	1029
Asp Leu Ala Cys Thr Pro Thr Asp Val Arg Asp Val Asp Ile	
285 290 295	
tgaggggccccc aggcaggcg ggccaccgc caccgcagc gagggcgagg ccggccccag	1089
gtgctccaca tgacagtccc tcctctccgg agcattttga taccagaagg gaaagcttca	1149
ttctccttgt tgttggttgt ttttcctt gctttccc cttccatct ctgacttaag	1209
caaaaagaaaa agattaccca aaaactgtct ttaaaagaga gagagag	1256

<210> 11
<211> 2121
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> (559) .. (1875)

<400> 11
 ctgctcgcgg ccgccaccgc cgggccccgg ccgtccctgg ctcccctcct gcctcgagaa 60
 gggcagggct ttcagaggc ttggcgggaa aaaagaacgg agggagggat cgcgctgagt 120
 ataaaagccg gtttcgggg ctttatctaa ctgcgtgtag taattccagc gagaggcaga 180
 gggagcgagc gggcgccgg ctagggtgga agagccgggc gagcagagct gcgctgcggg 240
 cgtcctggga agggagatcc ggagcgaata gggggcttcg cctctggccc agccctcccg 300
 cttgatcccc caggccagcg gtccgcaacc cttgccgcat ccacgaaact ttgcccata 360
 cagcgggcgg gcactttgca ctggaaactta caacacccga gcaaggacgc gactctcccg 420
 acgcggggag gctattctgc ccatttgggg acacttcccc gccgctgcca ggacccgctt 480
 ctctgaaagg ctctccttgc agctgcttag acgctggatt ttttcgggt agtggaaaac 540
 cagcagcctc ccgcgacg atg ccc ctc aac gtt agc ttc acc aac agg aac 591
 Met Pro Leu Asn Val Ser Phe Thr Asn Arg Asn
 1 5 10

tat gac ctc gac tac gac tcg gtg cag ccg tat ttc tac tgc gac gag 639
 Tyr Asp Leu Asp Tyr Asp Ser Val Gln Pro Tyr Phe Tyr Cys Asp Glu
 15 20 25

gag gag aac ttc tac cag cag cag cag agc gag ctg cag ccc ccg 687
 Glu Glu Asn Phe Tyr Gln Gln Gln Gln Ser Glu Leu Gln Pro Pro
 30 35 40

gcg ccc agc gag gat atc tgg aag aaa ttc gag ctg ctg ccc acc ccg 735
 Ala Pro Ser Glu Asp Ile Trp Lys Lys Phe Glu Leu Leu Pro Thr Pro
 45 50 55

ccc ctg tcc cct agc cgc cgc tcc ggg ctc tgc tcg ccc tcc tac gtt 783
 Pro Leu Ser Pro Ser Arg Arg Ser Gly Leu Cys Ser Pro Ser Tyr Val
 60 65 70 75

gcg gtc aca ccc ttc tcc ctt cgg gga gac aac gac ggc ggt ggc ggg 831
 Ala Val Thr Pro Phe Ser Leu Arg Gly Asp Asn Asp Gly Gly Gly
 80 85 90

agc ttc tcc acg gcc gac cag ctg gag atg gtg acc gag ctg ctg gga 879
 Ser Phe Ser Thr Ala Asp Gln Leu Glu Met Val Thr Glu Leu Leu Gly
 95 100 105

gga gac atg gtg aac cag agt ttc atc tgc gac ccg gac gac gag acc 927
 Gly Asp Met Val Asn Gln Ser Phe Ile Cys Asp Pro Asp Asp Glu Thr

110	115	120	
ttc atc aaa aac atc atc atc cag gac tgt atg tgg agc ggc ttc tcg Phe Ile Lys Asn Ile Ile Gln Asp Cys Met Trp Ser Gly Phe Ser	975		
125 130 135			
gcc gcc gcc aag ctc gtc tca gag aag ctg gcc tcc tac cag gct gcg Ala Ala Ala Lys Leu Val Ser Glu Lys Leu Ala Ser Tyr Gln Ala Ala	1023		
140 145 150 155			
cgc aaa gac agc ggc agc ccg aac ccc gcc cgc ggc cac agc gtc tgc Arg Lys Asp Ser Gly Ser Pro Asn Pro Ala Arg Gly His Ser Val Cys	1071		
160 165 170			
tcc acc tcc agc ttg tac ctg cag gat ctg agc gcc gcc gcc tca gag Ser Thr Ser Ser Leu Tyr Leu Gln Asp Leu Ser Ala Ala Ala Ser Glu	1119		
175 180 185			
tgc atc gac ccc tcg gtg gtc ttc ccc tac cct ctc aac gac agc agc Cys Ile Asp Pro Ser Val Val Phe Pro Tyr Pro Leu Asn Asp Ser Ser	1167		
190 195 200			
tcg ccc aag tcc tgc gcc tcg caa gac tcc agc gcc ttc tct ccg tcc Ser Pro Lys Ser Cys Ala Ser Gln Asp Ser Ser Ala Phe Ser Pro Ser	1215		
205 210 215			
tcg gat tct ctg ctc tcc tcg acg gag tcc tcc ccg cag ggc agc ccc Ser Asp Ser Leu Leu Ser Ser Thr Glu Ser Ser Pro Gln Gly Ser Pro	1263		
220 225 230 235			
gag ccc ctg gtg ctc cat gag gag aca ccg ccc acc acc agc agc gac Glu Pro Leu Val Leu His Glu Glu Thr Pro Pro Thr Thr Ser Ser Asp	1311		
240 245 250			
tct gag gag gaa caa gaa gat gag gaa gaa atc gat gtt gtt tct gtg Ser Glu Glu Glu Gln Glu Asp Glu Glu Ile Asp Val Val Ser Val	1359		
255 260 265			
gaa aag agg cag gct cct ggc aaa agg tca gag tct gga tca cct tct Glu Lys Arg Gln Ala Pro Gly Lys Arg Ser Glu Ser Gly Ser Pro Ser	1407		
270 275 280			
gct gga ggc cac agc aaa cct cct cac agc cca ctg gtc ctc aag agg Ala Gly Gly His Ser Lys Pro Pro His Ser Pro Leu Val Leu Lys Arg	1455		
285 290 295			
tgc cac gtc tcc aca cat cag cac aac tac gca gcg cct ccc tcc act Cys His Val Ser Thr His Gln His Asn Tyr Ala Ala Pro Pro Ser Thr	1503		
300 305 310 315			
cgg aag gac tat cct gct gcc aag agg gtc aag ttg gac agt gtc aga Arg Lys Asp Tyr Pro Ala Ala Lys Arg Val Lys Leu Asp Ser Val Arg	1551		
320 325 330			

gtc ctg aga cag atc agc aac cga aaa tgc acc agc ccc agg tcc		1599	
Val Leu Arg Gln Ile Ser Asn Asn Arg Lys Cys Thr Ser Pro Arg Ser			
335	340	345	
tcg gac acc gag gag aat gtc aag agg cga aca cac aac gtc ttg gag		1647	
Ser Asp Thr Glu Glu Asn Val Lys Arg Arg Thr His Asn Val Leu Glu			
350	355	360	
cgc cag agg agg aac gag cta aaa cg ^g agc ttt ttt gcc ctg cgt gac		1695	
Arg Gln Arg Arg Asn Glu Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp			
365	370	375	
cag atc ccg gag ttg gaa aac aat gaa aag gcc ccc aag gta gtt atc		1743	
Gln Ile Pro Glu Leu Glu Asn Asn Glu Lys Ala Pro Lys Val Val Ile			
380	385	390	395
ctt aaa aaa gcc aca gca tac atc ctg tcc gtc caa gca gag gag caa		1791	
Leu Lys Lys Ala Thr Ala Tyr Ile Leu Ser Val Gln Ala Glu Glu Gln			
400	405	410	
aag ctc att tct gaa gag gac ttg ttg cg ^g aaa cga cga gaa cag ttg		1839	
Lys Leu Ile Ser Glu Glu Asp Leu Leu Arg Lys Arg Arg Glu Gln Leu			
415	420	425	
aaa cac aaa ctt gaa cag cta cg ^g aac tct tgt gc ^g taaggaaaag		1885	
Lys His Lys Leu Glu Gln Leu Arg Asn Ser Cys Ala			
430	435		
taaggaaaac gattccttct aacagaaaatg tcctgagcaa tcacctatga acttgttca		1945	
aatgcatgat caaatgcaac ctcacaacct tggctgagtc ttgagactga aagat ^{ttagc}		2005	
cataatgtaa actgcctcaa attggacttt gggcataaaaa gaacttttt atgcttacca		2065	
tctttttttt ttctttaaca gatttgtatt taagaattgt ttttaaaaaa ttttaa		2121	

<210> 12
<211> 2098
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (79)..(570)

<400> 12
cctgccgaag tcagttcctt gtggagccgg agctggcg^{gc} ggattcgccg aggcac^{cg} 60
gcactcagag gaggcgcc atg tca gaa ccg gct ggg gat gtc cgt cag aac 111
Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn
1 5 10

cca tgc ggc agc aag gcc tgc cgc cgc ctc ttc ggc cca gtg gac agc	159
Pro Cys Gly Ser Lys Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser	
15 20 25	
 gag cag ctg agc cgc gac tgt gat gcg cta atg gcg ggc tgc atc cag	207
Glu Gln Leu Ser Arg Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln	
30 35 40	
 gag gcc cgt gag cga tgg aac ttc gac ttt gtc acc gag aca cca ctg	255
Glu Ala Arg Glu Arg Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu	
45 50 55	
 gag ggt gac ttc gcc tgg gag cgt gtg cgg ggc ctt ggc ctg ccc aag	303
Glu Gly Asp Phe Ala Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys	
60 65 70 75	
 ctc tac ctt ccc acg ggg ccc cgg cga ggc cgg gat gag ttg gga gga	351
Leu Tyr Leu Pro Thr Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly	
80 85 90	
 ggc agg cgg cct gcc acc tca cct gct ctg ctg cag ggg aca gca gag	399
Gly Arg Arg Pro Gly Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu	
95 100 105	
 gaa gac cat gtg gac ctg tca ctg tct tgt acc ctt gtg cct cgc tca	447
Glu Asp His Val Asp Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser	
110 115 120	
 ggg gag cag gct gaa ggg tcc cca ggt gga cct gga gac tct cag ggt	495
Gly Glu Gln Ala Glu Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly	
125 130 135	
 cga aaa cgg cgg cag acc agc atg aca gat ttc tac cac tcc aaa cgc	543
Arg Lys Arg Arg Gln Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg	
140 145 150 155	
 cg ^g ctg atc ttc tcc aag agg aag ccc taatccgccc acaggaagcc	590
Arg Leu Ile Phe Ser Lys Arg Lys Pro	
160	
 tgcagtcctg gaagcgcgag ggcctcaaag gccccgtcta catcttctgc ctttagtctca	650
gttttgttgt cttaattatt atttgtgttt taatttaaac acctcctcat gtacatacc	710
tggccgcccc ctgcccccca gcctctggca tttagaattat ttaaaacaaaa actaggcggt	770
tgaatgagag gttcctaaga gtgctggca tttttatattt atgaaatact atttaaagcc	830
tcctcatccc gtgttctcct tttcctctct cccggaggtt ggggtggccg gtttcatgcc	890
agctacttcc tcctccccac ttgtccgctg ggtggtaacc tctggaggggg tgggtttttt	950
tcccatcgct gtcacaggcg gttatgaaat tcacccctt tcctggacac tcagacctga	1010

attcttttc atttgagaag taaacagatg gcactttgaa ggggcctcac cgagtggggg 1070
 catcatcaa aactttggag tcccctcacc tcctctaagg ttgggcaggg tgaccctgaa 1130
 gtgagcacag ccttagggctg agctggggac ctggtaccct cctggctctt gataccccc 1190
 tctgtcttgt gaaggcaggg ggaaggtggg gtctggagc agaccacccc gcctgccctc 1250
 atggcccttc tgacctgcac tggggagccc gtctcagtgt tgagccttt ccctcttgg 1310
 ctccccgtta cctttgagg agccccagct acccttcttc tccagctggg ctctgcaatt 1370
 cccctctgtt gctgtccctc ccccttgccttca gtaccctctc agctccaggt 1430
 ggctctgagg tgcctgtccc acccccaccc ccagctcaat ggactggaag gggaaaggac 1490
 acacaagaag aagggcaccc tagttctacc tcagggcagct caagcagcga ccgccccctc 1550
 ctctagctgt gggggtgagg gtcccatgtg gtggcacagg cccccttgag tggggttatc 1610
 tctgtgttag gggtatatga tgggggagta gatcttctta ggagggagac actggcccct 1670
 caaatcgicc agcgacccctc ctcatccacc ccatccctcc ccagttcatt gcactttgat 1730
 tagcagcggc acaaggagtc agacattta agatggtggc agtagaggct atggacaggg 1790
 catgccacgt gggctcatat gggctggga gtagttgtct ttccctggcac taacgttgag 1850
 cccctggagg cactgaagtg cttagtgta ttggagtatt ggggtctgac cccaaacacc 1910
 ttccagctcc tgtaacatac tggcctggac tgtttctct cggctccccca tgtgtcctgg 1970
 ttccccgttcc tccacctaga ctgtaaacct ctcgagggca gggaccacac cctgtactgt 2030
 tctgtgtctt tcacagctcc tcccacaatg ctgatataca gcaggtgctc aataaacgat 2090
 tcttagtg 2098

```

<210> 13
<211> 827
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (256)..(570)

<400> 13
ggcacgagggc aaagggcggc gcagcggctg ccgagctcg ggctggagggc ggcgagaaca 60
tggtgcgca gttcttgggt accctccgga ttccggcgccg gtgcggcccg ccgcgagtga 120
  
```

gggtttcgt ggtcacatc tcgtggttca cgggggagtg ggcagcgcca ggggcgccc 180
 ccgctgtggc cctcgctgatgctactga ggagccagcg tcttagggcag cagccgcttc 240
 ctagaagacc aggtc atg atg atg ggc agc gcc cga gtg gcg gag ctg ctg 291
 Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu
 1 5 10
 ctg ctc cac ggc gcg gag ccc aac tgc gcc gac ccc gcc act ctc acc 339
 Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr
 15 20 25
 cga ccc gtg cac gac gct gcc cgg gag ggc ttc ctg gac acg ctg gtg 387
 Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
 30 35 40
 gtg ctg cac cgg gcc ggg gcg cgg ctg gac gtg cgc gat gcc tgg ggc 435
 Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
 45 50 55 60
 cgt ctg ccc gtg gac ctg gct gag gag ctg ggc cat cgc gat gtc gca 483
 Arg Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala
 65 70 75
 cgg tac ctg cgc gcg gct gcg ggg ggc acc aga ggc agt aac cat gcc 531
 Arg Tyr Leu Arg Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala
 80 85 90
 cgc ata gat gcc gcg gaa ggt ccc tca gac atc ccc gat tgaaagaacc 580
 Arg Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
 95 100 105
 agagaggctc tgagaaacctt ccggaaactt agatcatcag tcaccgaagg tcctacaggg 640
 ccacaactgc cccccccaca acccaccccg cttcgtagt tttcattttag aaaatagagc 700
 ttttaaaaat gtcctgcctt ttaacgtaga tatatgcctt cccccactac cgtaaatgtc 760
 catttatatac attttttata tattcttata aaaatgtaaa aaagaaaaaa aaaaaaaaaa 820
 aaaaaaaaaa 827

<210> 14
 <211> 1275
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (163)..(681)

<400> 14

cctccctacg ggcgcctccg gcagcccttc ccgcgtgcgc agggctcaga gccgttccga 60
gatcttggag gtccgggtgg gagtgggggt ggggtggggg tgggggtgaa ggtggggggc 120
ggcgcgctc aggaaaggcg ggtgcgcgcc tgccccggc ag atg ggc agg ggg 174
Met Gly Arg Gly
1
cg tgc gtg ggt ccc agt ctg cag tta agg ggg cag gag tgg cgc tgc 222
Arg Cys Val Gly Pro Ser Leu Gln Leu Arg Gly Gln Glu Trp Arg Cys
5 10 15 20
tca cct ctg gtg cca aag ggc gca gcg gct gcc gag ctc ggc cct 270
Ser Pro Leu Val Pro Lys Gly Gly Ala Ala Ala Ala Glu Leu Gly Pro
25 30 35
gga ggc ggc gag aac atg gtg cgc agg ttc ttg gtg acc ctc cgg att 318
Gly Gly Glu Asn Met Val Arg Arg Phe Leu Val Thr Leu Arg Ile
40 45 50
cg cgc gcg tgc ggc ccg cca gtg agg gtt ttc gtg gtt cac atc 366
Arg Arg Ala Cys Gly Pro Pro Arg Val Arg Val Phe Val Val His Ile
55 60 65
ccg cgg ctc acg ggg gag tgg gca gcg cca ggg gcg ccc gcc gct gtg 414
Pro Arg Leu Thr Gly Glu Trp Ala Ala Pro Gly Ala Pro Ala Ala Val
70 75 80
gcc ctc gtg ctg atg cta ctg agg agc cag cgt cta ggg cag cag cgc 462
Ala Leu Val Leu Met Leu Leu Arg Ser Gln Arg Leu Gly Gln Gln Pro
85 90 95 100
ctt cct aga aga cca ggt cat gat gat ggg cag cgc ccg agt ggc gga 510
Leu Pro Arg Arg Pro Gly His Asp Asp Gly Gln Arg Pro Ser Gly Gly
105 110 115
gct gct gct cca cgg cgc gga gcc caa ctg cgc cga ccc cgc cac 558
Ala Ala Ala Pro Arg Arg Gly Ala Gln Leu Arg Arg Pro Arg His
120 125 130
tct cac ccg acc cgt gca cga cgc tgc ccg gga ggg ctt cct gga cac 606
Ser His Pro Thr Arg Ala Arg Arg Cys Pro Gly Gly Leu Pro Gly His
135 140 145
gct ggt ggt gct gca ccc cgg ggc ggc gcg gct gga cgt gcg cga tgc 654
Ala Gly Ala Ala Pro Gly Arg Gly Ala Ala Gly Arg Ala Arg Cys
150 155 160
ctg ggg ccg tct gcc cgt gga cct ggc tgaggagctg ggccatcgcg 701
Leu Gly Pro Ser Ala Arg Gly Pro Gly
165 170
atatccacacq qtacacctqcac qcqqactqcqq qqqqcaccaq aqqcaqtaac catqcccqca 761

tagatgccgc ggaaggtccc tcagacatcc ccgattgaaa gaaccagaga ggctctgaga 821
 aacctcgaa aacttagatc atcagtacc gcaggccta cagggccaca actgcccccg 881
 ccacaaccca ccccgcttc gtagtttca ttttagaaaat agagctttta aaaatgtcct 941
 gcctttaac gtagatatac gccttcccc actaccgtaa atgtccattt atatcatttt 1001
 ttatataattc ttataaaaat gtaaaaaaga aaaacaccgc ttctgcctt tcactgtgtt 1061
 ggagtttct ggagttagca ctcacgcctt aagcgcacat tcatgtggc atttcttgcg 1121
 agcctcgca gctccgaaag ctgtcgactt catgacaagc attttgtaa ctaggaaagc 1181
 tcaggggggt tactggcttc tcttgagtca cactgctagc aaatggcaga accaaagctc 1241
 aaataaaaat aaaataattt tcattcattc actc 1275

<210> 15
 <211> 1850
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (213)..(1616)

<400> 15
 gggccaggct gaagctcagg gccctgtctg ctctgtggac tcaacagttt gtggcaagac 60
 aagctcagaa ctgagaagct gtcaccacag ttctggaggc tggaaagttc aagatcaaag 120
 tgccagcaga ttcaagtgtca tgtgaggacg tgcttcctgc ttcatagata agagcttgg 180
 gctcggcgca caaccagcac catctggtcg cg atg gtg gac acg gaa agc cca 233
 Met Val Asp Thr Glu Ser Pro
 1 5

ctc tgc ccc ctc tcc cca ctc gag gcc ggc gat cta gag agc ccg tta	281
Leu Cys Pro Leu Ser Pro Leu Glu Ala Gly Asp Leu Glu Ser Pro Leu	
10 15 20	

tct gaa gag ttc ctg caa gaa atg gga aac atc caa gag att tcg caa 329
 Ser Glu Glu Phe Leu Gln Glu Met Gly Asn Ile Gln Glu Ile Ser Gln
 25 30 35

tcc atc ggc gag gat agt tct gga agc ttt ggc ttt acg gaa tac cag	377
Ser Ile Gly Glu Asp Ser Ser Gly Ser Phe Gly Phe Thr Glu Tyr Gln	
40 45 50 55	

tat tta gga agc tgt cct ggc tca gat ggc tcg gtc atc acg gac acg 425
 Tyr Leu Gly Ser Cys Pro Gly Ser Asp Gly Ser Val Ile Thr Asp Thr

60.	65	70	
ctt tca cca gct tcg agc ccc tcc tcg gtg act tat cct gtg gtc ccc Leu Ser Pro Ala Ser Ser Pro Ser Ser Val Thr Tyr Pro Val Val Pro	75	80	473
ggc agc gtg gac gag tct ccc agt gga gca ttg aac atc gaa tgt aga Gly Ser Val Asp Glu Ser Pro Ser Gly Ala Leu Asn Ile Glu Cys Arg	90	95	521
atc tgc ggg gac aag gcc tca ggc tat cat tac gga gtc cac gcg tgt Ile Cys Gly Asp Lys Ala Ser Gly Tyr His Tyr Gly Val His Ala Cys	105	110	569
gaa ggc tgc aag ggc ttc ttt cgg cga acg att cga ctc aag ctg gtg Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Val	120	125	617
130		135	
tat gac aag tgc gac cgc agc tgc aag atc cag aaa aag aac aga aac Tyr Asp Lys Cys Asp Arg Ser Cys Lys Ile Gln Lys Lys Asn Arg Asn	140	145	665
150			
aaa tgc cag tat tgt cga ttt cac aag tgc ctt tct gtc ggg atg tca Lys Cys Gln Tyr Cys Arg Phe His Lys Cys Leu Ser Val Gly Met Ser	155	160	713
165			
cac aac gcg att cgt ttt gga cga atg cca aga tct gag aaa gca aaa His Asn Ala Ile Arg Phe Gly Arg Met Pro Arg Ser Glu Lys Ala Lys	170	175	761
180			
ctg aaa gca gaa att ctt acc tgt gaa cat gac ata gaa gat tct gaa Leu Lys Ala Glu Ile Leu Thr Cys Glu His Asp Ile Glu Asp Ser Glu	185	190	809
195			
act gca gat ctc aaa tct ctg gcc aag aga atc tac gag gcc tac ttg Thr Ala Asp Leu Lys Ser Leu Ala Lys Arg Ile Tyr Glu Ala Tyr Leu	200	205	857
210		215	
aag aac ttc aac atg aac aag gtc aaa gcc cgg gtc atc ctc tca gga Lys Asn Phe Asn Met Asn Lys Val Lys Ala Arg Val Ile Leu Ser Gly	220	225	905
230			
aag gcc agt aac aat cca cct ttt gtc ata cat gat atg gag aca ctg Lys Ala Ser Asn Asn Pro Pro Phe Val Ile His Asp Met Glu Thr Leu	235	240	953
245			
tgt atg gct gag aag acg ctg gtg gcc aag ctg gtg gcc aat ggc atc Cys Met Ala Glu Lys Thr Leu Val Ala Lys Leu Val Ala Asn Gly Ile	250	255	1001
260			
cag aac aag gag gcg gag gtc cgc atc ttt cac tgc tgc cag tgc acg Gln Asn Lys Glu Ala Glu Val Arg Ile Phe His Cys Cys Gln Cys Thr	265	270	1049
275			

tca	gtg	gag	acc	gtc	acg	gag	ctc	acg	gaa	ttc	gcc	aag	gcc	atc	cca	1097					
Ser	Val	Glu	Thr	Val	Thr	Glu	Leu	Thr	Glu	Phe	Ala	Lys	Ala	Ile	Pro						
280		285				290			295												
ggc	ttc	gca	aac	ttg	gac	ctg	aac	gat	caa	gtg	aca	ttg	cta	aaa	tac	1145					
Gly	Phe	Ala	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr						
300		305				310															
gga	gtt	tat	gag	gcc	ata	ttc	gcc	atg	ctg	tct	tct	gtg	atg	aac	aaa	1193					
Gly	Val	Tyr	Glu	Ala	Ile	Phe	Ala	Met	Leu	Ser	Ser	Val	Met	Asn	Lys						
315			320			325															
gac	ggg	atg	ctg	gta	gcg	tat	gga	aat	ggg	ttt	ata	act	cgt	gaa	ttc	1241					
Asp	Gly	Met	Leu	Val	Ala	Tyr	Gly	Asn	Gly	Phe	Ile	Thr	Arg	Glu	Phe						
330		335		340																	
cta	aaa	agc	cta	agg	aaa	ccg	ttc	tgt	gat	atc	atg	gaa	ccc	aag	ttt	1289					
Leu	Lys	Ser	Leu	Arg	Lys	Pro	Phe	Cys	Asp	Ile	Met	Glu	Pro	Lys	Phe						
345		350		355																	
gat	ttt	gcc	atg	aag	ttc	aat	gca	ctg	gaa	ctg	gat	gac	agt	gat	atc	1337					
Asp	Phe	Ala	Met	Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	Ile						
360		365		370		375															
tcc	ctt	ttt	gtg	gct	gct	atc	att	tgc	tgt	gga	gat	cgt	cct	ggc	ctt	1385					
Ser	Leu	Phe	Val	Ala	Ala	Ile	Ile	Cys	Cys	Gly	Asp	Arg	Pro	Gly	Leu						
380		385		390																	
cta	aac	gta	gga	cac	att	gaa	aaa	atg	cag	gag	ggt	att	gta	cat	gtg	1433					
Leu	Asn	Val	Gly	His	Ile	Glu	Lys	Met	Gln	Glu	Gly	Ile	Val	His	Val						
395		400		405																	
ctc	aga	ctc	cac	ctg	cag	agc	aac	cac	ccg	gac	gat	atc	ttt	ctc	ttc	1481					
Leu	Arg	Leu	His	Leu	Gln	Ser	Asn	His	Pro	Asp	Asp	Ile	Phe	Leu	Phe						
410		415		420																	
cca	aaa	ctt	ctt	caa	aaa	atg	gca	gac	ctc	cg	cag	ctg	gtg	acg	gag	1529					
Pro	Lys	Leu	Leu	Gln	Lys	Met	Ala	Asp	Leu	Arg	Gln	Leu	Val	Thr	Glu						
425		430		435																	
cat	gcg	cag	ctg	gtg	cag	atc	atc	aag	aag	acg	gag	tcg	gat	gct	gcg	1577					
His	Ala	Gln	Leu	Val	Gln	Ile	Ile	Lys	Lys	Thr	Glu	Ser	Asp	Ala	Ala						
440		445		450		455															
ctg	cac	ccg	cta	ctg	cag	gag	atc	tac	agg	gac	atg	tac	tgagttcctt		1626						
Leu	His	Pro	Leu	Leu	Gln	Ile	Tyr	Arg	Asp	Met	Tyr										
460		465																			
cagatcagcc	acac	ctt	ttc	cagg	ttct	gaag	ctg	aca	gc	act	aca	aa	gg	ag	ac	gggg	1686				
gagc	cagc	ac	ttt	gc	caca	aat	at	cc	acc	act	tta	ac	tag	ctt	gg	ac	gt	ct	gag	1746	
ctgt	agg	taa	cc	gg	ccat	at	tt	ccat	at	tt	ttt	aa	cc	ag	t	tc	ta	ag	ac	ta	1806

gaactcaaat gctgggggag gtggctaata tcaggactgg gaag 1850
 <210> 16
 <211> 1609
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (92) .. (1606)
 <400> 16
 ttcaagtctt tttcttttaa cggattgatc ttttgctaga tagagacaaa atatcagtgt 60
 gaattacagc aaacccctat tccatgctgt t atg ggt gaa act ctg gga gat 112
 Met Gly Glu Thr Leu Gly Asp
 1 5
 tct cct att gac cca gaa agc gat tcc ttc act gat aca ctg tct gca 160
 Ser Pro Ile Asp Pro Glu Ser Asp Ser Phe Thr Asp Thr Leu Ser Ala
 10 15 20
 aac ata tca caa gaa atg acc atg gtt gac aca gag atg cca ttc tgg 208
 Asn Ile Ser Gln Glu Met Thr Met Val Asp Thr Glu Met Pro Phe Trp
 25 30 35
 ccc acc aac ttt ggg atc agc tcc gtg gat ctc tcc gta atg gaa gac 256
 Pro Thr Asn Phe Gly Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp
 40 45 50 55
 cac tcc cac tcc ttt gat atc aag ccc ttc act act gtt gac ttc tcc 304
 His Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser
 60 65 70
 agc att tct act cca cat tac gaa gac att cca ttc aca aga aca gat 352
 Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe Thr Arg Thr Asp
 75 80 85
 cca gtg gtt gca gat tac aag tat gac ctg aaa ctt caa gag tac caa 400
 Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu Gln Glu Tyr Gln
 90 95 100
 agt gca atc aaa gtg gag cct gca tct cca cct tat tat tct gag aag 448
 Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr Tyr Ser Glu Lys
 105 110 115
 act cag ctc tac aat aag cct cat gaa gag cct tcc aac tcc ctc atg 496
 Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser Asn Ser Leu Met
 120 125 130 135
 gca att gaa tgt cgt gtc tgt gga gat aaa gct tct gga ttt cac tat 544
 Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr

140	145	150	
gga gtt cat gct tgt gaa gga tgc aag ggt ttc ttc cgg aga aca atc Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile 155	160	165	592
aga ttg aag ctt atc tat gac aga tgt gat ctt aac tgt cgg atc cac Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp Leu Asn Cys Arg Ile His 170	175	180	640
aaa aaa agt aga aat aaa tgt cag tac tgt cgg ttt cag aaa tgc ctt Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu 185	190	195	688
gca gtg ggg atg tct cat aat gcc atc agg ttt ggg cgg atg cca cag Ala Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Gln 200	205	210	736
gcc gag aag gag aag ctg ttg gcg gag atc tcc agt gat atc gac cag Ala Glu Lys Glu Lys Leu Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln 220	225	230	784
ctg aat cca gag tcc gct gac ctc cgg gcc ctg gca aaa cat ttg tat Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr 235	240	245	832
gac tca tac ata aag tcc ttc ccg ctg acc aaa gca aag gcg agg gcg Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala 250	255	260	880
atc ttg aca gga aag aca aca gac aaa tca cca ttc gtt atc tat gac Ile Leu Thr Gly Lys Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp 265	270	275	928
atg aat tcc tta atg atg gga gaa gat aaa atc aag ttc aaa cac atc Met Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile 280	285	290	976
acc ccc ctg cag gag cag agc aaa gag gtg gcc atc cgc atc ttt cag Thr Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln 300	305	310	1024
ggc tgc cag ttt cgc tcc gtg gag gct gtg cag gag atc aca gag tat Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr 315	320	325	1072
gcc aaa agc att cct ggt ttt gta aat ctt gac ttg aac gac caa gta Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val 330	335	340	1120
act ctc ctc aaa tat gga gtc cac gag atc att tac aca atg ctg gcc Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala 345	350	355	1168

tcc ttg atg aat aaa gat ggg gtt ctc ata tcc gag ggc caa ggc ttc	1216
Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe	
360 365 370 375	
atg aca agg gag ttt cta aag agc ctg cga aag cct ttt ggt gac ttt	1264
Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe	
380 385 390	
atg gag ccc aag ttt gag ttt gct gtg aag ttc aat gca ctg gaa tta	1312
Met Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu	
395 400 405	
gat gac agc gac ttg gca ata ttt att gct gtc att att ctc agt gga	1360
Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly	
410 415 420	
gac cgc cca ggt ttg ctg aat gtg aag ccc att gaa gac att caa gac	1408
Asp Arg Pro Gly Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp	
425 430 435	
aac ctg cta caa gcc ctg gag ctc cag ctg aag ctg aac cac cct gag	1456
Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu	
440 445 450 455	
tcc tca cag ctg ttt gcc aag ctg ctc cag aaa atg aca gac ctc aga	1504
Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg	
460 465 470	
cag att gtc acg gaa cac gtg cag cta ctg cag gtg atc aag aag acg	1552
Gln Ile Val Thr Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr	
475 480 485	
gag aca gac atg agt ctt cac ccg ctc ctg cag gag atc tac aag gac	1600
Glu Thr Asp Met Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp	
490 495 500	
ttg tac tag	1609
Leu Tyr	
505	

```

<210> 17
<211> 3301
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (338)..(1660)

<220>
<221> modified_base
<222> (2966)..(2972)

```

<223> a, c, t, g, other, or unknown

<400> 17

gaattctgcg gaggcctgcgg gacggcgccg gggttggcccg taggcagccg ggacagtgtt 60
 gtacagtgtt ttgggcatgc acgtgatact cacacagtgg cttctgctca ccaacagatg 120
 aagacagatg caccaacgag ggtctggaaat ggtctggagt ggtctggaaa gcagggtcag 180
 ataccctgg aaaactgaag cccgtggagc aatgatctct acaggactgc ttcaaggctg 240
 atgggaacca ccctgttagag gtccatctgc gttcagaccc agacgatgcc agagctatga 300
 ctgggcctgc aggtgtggcg ccgaggggag atcagcc atg gag cag cca cag gag 355
 Met Glu Gln Pro Gln Glu
 1 5

1
 gaa gcc cct gag gtc cgg gaa gag gag gag aaa gag gaa gtg gca gag 403
 Glu Ala Pro Glu Val Arg Glu Glu Glu Lys Glu Val Ala Glu
 10 15 20

gca gaa gga gcc cca gag ctc aat ggg gga cca cag cat gca ctt cct 451
 Ala Glu Gly Ala Pro Glu Leu Asn Gly Gly Pro Gln His Ala Leu Pro
 25 30 35

tcc agc agc tac aca gac ctc tcc cgg agc tcc tcg cca ccc tca ctg 499
 Ser Ser Tyr Thr Asp Leu Ser Arg Ser Ser Pro Pro Ser Leu
 40 45 50

ctg gac caa ctg cag atg ggc tgt gac ggg gcc tca tgc ggc agc ctc 547
 Leu Asp Gln Leu Gln Met Gly Cys Asp Gly Ala Ser Cys Gly Ser Leu
 55 60 65 70

aac atg gag tgc cgg gtg tgc ggg gac aag gca tcg ggc ttc cac tac 595
 Asn Met Glu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr
 75 80 85

ggt gtt cat gca tgt gag ggg tgc aag ggc ttc ttc cgt cgt acg atc 643
 Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile
 90 95 100

cgc atg aag ctg gag tac gag aag tgt gag cgc agc tgc aag att cag 691
 Arg Met Lys Leu Glu Tyr Glu Lys Cys Glu Arg Ser Cys Lys Ile Gln
 105 110 115

aag aag aac cgc aac aag tgc cag tac tgc cgc ttc cag aag tgc ctg 739
 Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu
 120 125 130

gca ctg ggc atg tca cac aac gct atc cgt ttt ggt cgg atg ccg gag 787
 Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Glu
 135 140 145 150

gct gag aag agg aag ctg gtg gca ggg ctg act gca aac gag ggg agc 835

Ala Glu Lys Arg Lys Leu Val Ala Gly Leu Thr Ala Asn Glu Gly Ser			
155	160	165	
cag tac aac cca cag gtg gcc gac ctg aag gcc ttc tcc aag cac atc			883
Gln Tyr Asn Pro Gln Val Ala Asp Leu Lys Ala Phe Ser Lys His Ile			
170	175	180	
tac aat gcc tac ctg aaa aac ttc aac atg acc aaa aag aag gcc cgc			931
Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met Thr Lys Lys Ala Arg			
185	190	195	
agc atc ctc acc ggc aaa gcc agc cac acg gcg ccc ttt gtg atc cac			979
Ser Ile Leu Thr Gly Lys Ala Ser His Thr Ala Pro Phe Val Ile His			
200	205	210	
gac atc gag aca ttg tgg cag gca gag aag ggg ctg gtg tgg aag cag			1027
Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys Gly Leu Val Trp Lys Gln			
215	220	225	230
ttg gtg aat ggc ctg cct ccc tac aag gag atc agc gtg cac gtc ttc			1075
Leu Val Asn Gly Leu Pro Pro Tyr Lys Glu Ile Ser Val His Val Phe			
235	240	245	
tac cgc tgc cag tgc acc aca gtg gag acc gtg cgg gag ctc act gag			1123
Tyr Arg Cys Gln Cys Thr Thr Val Glu Thr Val Arg Glu Leu Thr Glu			
250	255	260	
ttc gcc aag agc atc ccc agc ttc agc agc ctc ttc ctc aac gac cag			1171
Phe Ala Lys Ser Ile Pro Ser Phe Ser Ser Leu Phe Leu Asn Asp Gln			
265	270	275	
gtt acc ctt ctc aag tat ggc gtg cac gag gcc atc ttc gcc atg ctg			1219
Val Thr Leu Leu Lys Tyr Gly Val His Glu Ala Ile Phe Ala Met Leu			
280	285	290	
gcc tct atc gtc aac aag gac ggg ctg ctg gta gcc aac ggc agt ggc			1267
Ala Ser Ile Val Asn Lys Asp Gly Leu Leu Val Ala Asn Gly Ser Gly			
295	300	305	310
ttt gtc acc cgt gag ttc ctg cgc agc ctc cgc aaa ccc ttc agt gat			1315
Phe Val Thr Arg Glu Phe Leu Arg Ser Leu Arg Lys Pro Phe Ser Asp			
315	320	325	
atc att gag cct aag ttt gaa ttt gct gtc aag ttc aac gcc ctg gaa			1363
Ile Ile Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu			
330	335	340	
ctt gat gac agt gac ctg gcc cta ttc att gcg gcc atc att ctg tgt			1411
Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile Ala Ala Ile Ile Leu Cys			
345	350	355	
gga gac cgg cca ggc ctc atg aac gtt cca cgg gtg gag gct atc cag			1459
Gly Asp Arg Pro Gly Leu Met Asn Val Pro Arg Val Glu Ala Ile Gln			
360	365	370	

gac acc atc ctg cgt gcc ctc gaa ttc cac ctg cag gcc aac cac cct		1507
Asp Thr Ile Leu Arg Ala Leu Glu Phe His Leu Gln Ala Asn His Pro		
375	380	385
390		
gat gcc cag tac ctc ttc ccc aag ctg ctg cag aag atg gct gac ctg		1555
Asp Ala Gln Tyr Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp Leu		
395	400	405
cgg caa ctg gtc acc gag cac gcc cag atg atg cag cgg atc aag aag		1603
Arg Gln Leu Val Thr Glu His Ala Gln Met Met Gln Arg Ile Lys Lys		
410	415	420
acc gaa acc gag acc tcg ctg cac cct ctg ctc cag gag atc tac aag		1651
Thr Glu Thr Glu Thr Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys		
425	430	435
gac atg tac taacggcggc acccaggcct ccctgcagac tccaatgggg		1700
Asp Met Tyr		
440		
ccagcactgg aggggcccac ccacatgact ttccattga ccagctctct tcctgtcttt		1760
gttgtctccc tcttctcag ttcccttttc ttttctaatt cctgttgctc tgtttcttcc		1820
tttctgttagg tttctctctt cccttctccc ttctcccttg ccctcccttt ctctctccta		1880
tccccacgtc tgtccctcctt tcttattctg tgagatgttt tgtattattt caccagcagc		1940
atagaacagg acctctgctt ttgcacacct tttccccagg agcagaagag agtgggcctg		2000
ccctctgccc catcattgca cctgcaggct taggtcctca cttctgtctc ctgtcttcag		2060
agcaaaaagac ttgagccatc caaagaaaca ctaagctctc tgggcctggg ttccagggaa		2120
ggctaagcat ggcctggact gactgcagcc ccctatagtc atggggtccc tgctgcaaag		2180
gacagtggca gacccggca gtagagccga gatgcctccc caagactgtc attgcccctc		2240
cgatcgtgag gccacccact gacccaatga tcctctccag cagcacacct cagccccact		2300
gacacccagt gtcctccat cttcacactg gttgccagg ccaatgtgc tcatggcccc		2360
tccagcacac acacataagc actgaaatca ctttacactgc aggcaccatg cacccctt		2420
ccctccctga ggcaggtgag aacccagaga gaggggcctg caggtgagca ggcaggcgtg		2480
ggccaggtct cgggggaggc aggggtcctg caggtcctgg tgggtcagcc cagcacctcg		2540
cccagtggga gttccccggg ataaactgag cctgttcatt ctgtatgtcca ttgtcccaa		2600
tagctctact gccctccct tccccttac tcagcccagc tggccaccta gaagtctccc		2660
tgcacagcct ctagtgtccg gggaccttgt gggaccagtc ccacaccgct ggtccctgcc		2720

ctccccctgct cccaggttga ggtgcgctca cctcagagca gggccaaagc acagctggc 2780
atgccatgtc tgagcggcgc agagccctcc aggccctgcag gggcaagggg ctggctggag 2840
tctcagagca cagaggtagg agaactgggg ttcaagccca ggcttcctgg gtcctgcctg 2900
gtcctccctc ccaaggagcc attctatgtg actctgggtg gaagtgcacca gcccctgcct 2960
gacggnnnnn nngatcaactc tctgctggca ggattcttcc cgctccccac ctaccagct 3020
gatgggggtt ggggtgcttc tttcagccaa ggctatgaag ggacagctgc tgggacccac 3080
ctccccccctt cccccggccac atgccgcgtc cctgccccca cccgggtctg gtgctgagga 3140
tacagctctt ctcagtgtct gaacaatctc caaaaattgaa atgtatattt ttgcttaggag 3200
ccccagcttc ctgtgttttt aatataaata gtgtacacag actgacgaaa ctttaataaa 3260
atgggaatta aatatttaaa aaaaaaagcg gccgcgaatt c 3301

```
<210> 18  
<211> 3083  
<212> DNA  
<213> Homo sapiens
```

<220>
<221> CDS
<222> (162) . . (2387)

```
<400> 18
aaaaactgca gccaaacttcc gaggcagcct cattgcccaag cggaaccccaag cctctgccag 60
gttcgggtcccg ccatcctcg t cccgtcctcc gcccggccct gccccgcgcc cagggatcct 120
ccagctcctt tcgccccgcgc cctccgttcg ctccggacac c atg gac aag ttt tgg 176
                                         Met Asp Lys Phe Trp
                                         1           5
```

```

tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg agc ctg gcg cag 224
Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu Ser Leu Ala Gln
          10           15           20

```

atc gat ttg aat ata acc tgc cgc ttt gca ggt gta ttc cac gtg gag 272
 Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val Phe His Val Glu
 25 30 35

aaq qct ttc aat aqc acc ttq ccc aca atq qcc caq atq qag aaa qct 368

Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln Met Glu Lys Ala			
55	60	65	
ctg agc atc gga ttt gag acc tgc agg tat ggg ttc ata gaa ggg cac			416
Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe Ile Glu Gly His			
70	75	80	85
gtg gtg att ccc cg ^g atc cac ccc aac tcc atc tgt gca gca aac aac			464
Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys Ala Ala Asn Asn			
90	95		100
aca ggg gtg tac atc ctc aca tcc aac acc tcc cag tat gac aca tat			512
Thr Gly Val Tyr Ile Leu Thr Ser Asn Thr Ser Gln Tyr Asp Thr Tyr			
105	110	115	
tgc ttc aat gct tca gct cca cct gaa gaa gat tgt aca tca gtc aca			560
Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys Thr Ser Val Thr			
120	125	130	
gac ctg ccc aat gcc ttt gat gga cca att acc ata act att gtt aac			608
Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile Thr Ile Val Asn			
135	140	145	
cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac aga acg aat cct			656
Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr Arg Thr Asn Pro			
150	155	160	165
gaa gac atc tac ccc agc aac cct act gat gat gac gtg agc agc ggc			704
Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp Val Ser Ser Gly			
170	175	180	
tcc tcc agt gaa agg agc agc act tca gga ggt tac atc ttt tac acc			752
Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr Ile Phe Tyr Thr			
185	190	195	
ttt tct act gta cac ccc atc cca gac gaa gac agt ccc tgg atc acc			800
Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser Pro Trp Ile Thr			
200	205	210	
gac agc aca gac aga atc cct gct acc act ttg atg agc act agt gct			848
Asp Ser Thr Asp Arg Ile Pro Ala Thr Thr Leu Met Ser Thr Ser Ala			
215	220	225	
aca gca act gag aca gca acc aag agg caa gaa acc tgg gat tgg ttt			896
Thr Ala Thr Glu Thr Ala Thr Lys Arg Gln Glu Thr Trp Asp Trp Phe			
230	235	240	245
tca tgg ttg ttt cta cca tca gag tca aag aat cat ctt cac aca aca			944
Ser Trp Leu Phe Leu Pro Ser Glu Ser Lys Asn His Leu His Thr Thr			
250	255	260	
aca caa atg gct ggt acg tct tca aat acc atc tca gca ggc tgg gag			992
Thr Gln Met Ala Gly Thr Ser Ser Asn Thr Ile Ser Ala Gly Trp Glu			
265	270	275	

cca aat gaa gaa aat gaa gat gaa aga gac aga cac ctc agt ttt tct		1040	
Pro Asn Glu Glu Asn Glu Asp Glu Arg Asp Arg His Leu Ser Phe Ser			
280	285	290	
gga tca ggc att gat gat gat gaa gat ttt atc tcc agc acc att tca		1088	
Gly Ser Gly Ile Asp Asp Asp Glu Asp Phe Ile Ser Ser Thr Ile Ser			
295	300	305	
acc aca cca cg ^g gct ttt gac cac aca aaa cag aac cag gac tgg acc		1136	
Thr Thr Pro Arg Ala Phe Asp His Thr Lys Gln Asn Gln Asp Trp Thr			
310	315	320	325
cag tgg aac cca agc cat tca aat ccg gaa gtg cta ctt cag aca acc		1184	
Gln Trp Asn Pro Ser His Ser Asn Pro Glu Val Leu Leu Gln Thr Thr			
330	335	340	
aca agg atg act gat gta gac aga aat ggc acc act gct tat gaa gga		1232	
Thr Arg Met Thr Asp Val Asp Arg Asn Gly Thr Thr Ala Tyr Glu Gly			
345	350	355	
aac tgg aac cca gaa gca cac cct ccc ctc att cac cat gag cat cat		1280	
Asn Trp Asn Pro Glu Ala His Pro Pro Leu Ile His His Glu His His			
360	365	370	
gag gaa gag acc cca cat tct aca agc aca atc cag gca act cct		1328	
Glu Glu Glu Thr Pro His Ser Thr Ser Thr Ile Gln Ala Thr Pro			
375	380	385	
agt agt aca acg gaa aca gct acc cag aag gaa cag tgg ttt ggc		1376	
Ser Ser Thr Thr Glu Glu Thr Ala Thr Gln Lys Glu Gln Trp Phe Gly			
390	395	400	405
aac aga tgg cat gag gga tat cgc caa aca ccc aaa gaa gac tcc cat		1424	
Asn Arg Trp His Glu Gly Tyr Arg Gln Thr Pro Lys Glu Asp Ser His			
410	415	420	
tcg aca aca ggg aca gct gca gcc tca gct cat acc agc cat cca atg		1472	
Ser Thr Thr Gly Thr Ala Ala Ala Ser Ala His Thr Ser His Pro Met			
425	430	435	
caa gga agg aca aca cca agc cca gag gac agt tcc tgg act gat ttc		1520	
Gln Gly Arg Thr Thr Pro Ser Pro Glu Asp Ser Ser Trp Thr Asp Phe			
440	445	450	
tcc aac cca atc tca cac ccc atg gga cga ggt cat caa gca gga aga		1568	
Phe Asn Pro Ile Ser His Pro Met Gly Arg Gly His Gln Ala Gly Arg			
455	460	465	
agg atg gat atg gac tcc agt cat agt ata acg ctt cag cct act gca		1616	
Arg Met Asp Met Asp Ser Ser His Ser Ile Thr Leu Gln Pro Thr Ala			
470	475	480	485
aat cca aac aca ggt ttg gtg gaa gat ttg gac agg aca gga cct ctt		1664	

Asn Pro Asn Thr Gly Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu			
490	495	500	
tca atg aca acg cag cag agt aat tct cag agc ttc tct aca tca cat			1712
Ser Met Thr Thr Gln Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His			
505	510	515	
gaa ggc ttg gaa gaa gat aaa gac cat cca aca act tct act ctg aca			1760
Glu Gly Leu Glu Glu Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr			
520	525	530	
tca agc aat agg aat gat gtc aca ggt gga aga aga gac cca aat cat			1808
Ser Ser Asn Arg Asn Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His			
535	540	545	
tct gaa ggc tca act act tta ctg gaa ggt tat acc tct cat tac cca			1856
Ser Glu Gly Ser Thr Thr Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro			
550	555	560	565
cac acg aag gaa agc agg acc ttc atc cca gtg acc tca gct aag act			1904
His Thr Lys Glu Ser Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr			
570	575	580	
ggg tcc ttt gga gtt act gca gtt act gtt gga gat tcc aac tct aat			1952
Gly Ser Phe Gly Val Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn			
585	590	595	
gtc aat cgt tcc tta tca gga gac caa gac aca ttc cac ccc agt ggg			2000
Val Asn Arg Ser Leu Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly			
600	605	610	
ggg tcc cat acc act cat gga tct gaa tca gat gga cac tca cat ggg			2048
Gly Ser His Thr Thr His Gly Ser Glu Ser Asp Gly His Ser His Gly			
615	620	625	
agt caa gaa ggt gga gca aac aca acc tct ggt cct ata agg aca ccc			2096
Ser Gln Glu Gly Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro			
630	635	640	645
caa att cca gaa tgg ctg atc ttg gca tcc ctc ttg gcc ttg gct			2144
Gln Ile Pro Glu Trp Leu Ile Leu Ala Ser Leu Leu Ala Leu Ala			
650	655	660	
ttg att ctt gca gtt tgc att gca gtc aac agt cga aga agg tgt ggg			2192
Leu Ile Leu Ala Val Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly			
665	670	675	
cag aag aaa aag cta gtg atc aac agt ggc aat gga gct gtg gag gac			2240
Gln Lys Lys Lys Leu Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp			
680	685	690	
aga aag cca agt gga ctc aac gga gag gcc agc aag tct cag gaa atg			2288
Arg Lys Pro Ser Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met			
695	700	705	

gtg cat ttg gtg aac aag gag tcg tca gaa act cca gac cag ttt atg	2336
Val His Leu Val Asn Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met	
710 715 720 725	
aca gct gat gag aca agg aac ctg cag aat gtg gac atg aag att ggg	2384
Thr Ala Asp Glu Thr Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly	
730 735 740	
gtg taacacctac accattatct tggaaagaaa caaccgttgg aaacataacc	2437
Val	
attacaggga gctgggacac ttaacagatg caatgtgcta ctgattgttt cattgcgaat	2497
cttttttagc ataaaaatttt ctactcttt tgtttttgt gttttttct ttaaagtca	2557
gtccaatttg taaaaacagc attgcttct gaaatttaggg cccaaattaat aatcagcaag	2617
aatttgcattt ttccagttcc cacttggagg ccttcatcc ctgggtgtg ctatggatgg	2677
cattctaaaca aaactacaca tatgtattcc tgatgccaa cctttcccc accagctaag	2737
gacatttccc agggtaata gggcctggc cctgggagga aatttgaatg ggtccatttt	2797
gcccttccat agcctaattcc ctgggcattt cttccactg aggttggggg ttgggtgt	2857
ctagttcacac atcttcaaca gacccctct agaaatttt cagatgttc tggagacac	2917
ccaaagggtg aagctattta tctgttagaa actatattc tgtgttttg aaatattaaa	2977
ccctggatca gtccttgat cagtataatt tttaaagtt actttgcag aggcacaaaa	3037
gggtttaaac tgattcataa taaatatctg tacttctcg atcttc	3083

```

<210> 19
<211> 2539
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (321)..(1787)

<400> 19
ggagtctctt gctctggttc ttgctgttcc tgctcctgct cccgcccgtc cccgtcctgc 60
tcgcggaccc agggcgccc acgccagtga atccctgttg ttactatcca tgccagcacc 120
agggcatctg tgtccgccttc ggccttgacc gctaccagtg tgactgcacc cgacacggct 180
attccggccc caactgcacc atccctggcc tgtggacctg gctccggaat tcactgcggc 240

```

ccagcccctc tttcacccac ttccctgctca ctcacggcg ctgggtctgg gagtttgtca 300
 atgccaccaa catccgagag atg ctc atg cgc ctg gta ctc aca gtg cgc tcc 353
 Met Leu Met Arg Leu Val Leu Thr Val Arg Ser
 1 5 10
 aac ctt atc ccc agt ccc acc tac aac tca gca cat gac tac atc 401
 Asn Leu Ile Pro Ser Pro Pro Thr Tyr Asn Ser Ala His Asp Tyr Ile
 15 20 25
 agc tgg gag tct ttc tcc aac gtg agc tat tac act cgt att ctg ccc 449
 Ser Trp Glu Ser Phe Ser Asn Val Ser Tyr Tyr Thr Arg Ile Leu Pro
 30 35 40
 tct gtg cct aaa gat tgc ccc aca ccc atg gga acc aaa ggg aag aag 497
 Ser Val Pro Lys Asp Cys Pro Thr Pro Met Gly Thr Lys Gly Lys Lys
 45 50 55
 cag ttg cca gat gcc cag ctc ctg gcc cgc ttc ctg ctc agg agg 545
 Gln Leu Pro Asp Ala Gln Leu Ala Arg Arg Phe Leu Leu Arg Arg
 60 65 70 75
 aag ttc ata cct gac ccc caa ggc acc aac ctc atg ttt gcc ttc ttt 593
 Lys Phe Ile Pro Asp Pro Gln Gly Thr Asn Leu Met Phe Ala Phe Phe
 80 85 90
 gca caa cac ttc acc cac cag ttc ttc aaa act tct ggc aag atg ggt 641
 Ala Gln His Phe Thr His Gln Phe Phe Lys Thr Ser Gly Lys Met Gly
 95 100 105
 cct ggc ttc acc aag gcc ttg ggc cat ggg gta gac ctc ggc cac att 689
 Pro Gly Phe Thr Lys Ala Leu Gly His Gly Val Asp Leu Gly His Ile
 110 115 120
 tat gga gac aat ctg gag cgt cag tat caa ctg cgg ctc ttt aag gat 737
 Tyr Gly Asp Asn Leu Glu Arg Gln Tyr Gln Leu Arg Leu Phe Lys Asp
 125 130 135
 ggg aaa ctc aag tac cag gtg ctg gat gga gaa atg tac ccg ccc tcg 785
 Gly Lys Leu Lys Tyr Gln Val Leu Asp Gly Glu Met Tyr Pro Pro Ser
 140 145 150 155
 gta gaa gag gcg cct gtg ttg atg cac tac ccc cga ggc atc ccg ccc 833
 Val Glu Glu Ala Pro Val Leu Met His Tyr Pro Arg Gly Ile Pro Pro
 160 165 170
 cag agc cag atg gct gtg ggc cag gag gtg ttt ggg ctg ctt cct ggg 881
 Gln Ser Gln Met Ala Val Gly Gln Glu Val Phe Gly Leu Leu Pro Gly
 175 180 185
 ctc atg ctg tat gcc acg ctc tgg cta cgt gag cac aac cgt gtg tgt 929
 Leu Met Leu Tyr Ala Thr Leu Trp Leu Arg Glu His Asn Arg Val Cys
 190 195 200

gac ctg ctg aag gct gag cac ccc acc tgg ggc gat gag cag ctt ttc		977	
Asp Leu Leu Lys Ala Glu His Pro Thr Trp Gly Asp Glu Gln Leu Phe			
205	210	215	
cag acg acc cgc ctc atc ctc ata ggg gag acc atc aag att gtc atc		1025	
Gln Thr Thr Arg Leu Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile			
220	225	230	235
gag gag tac gtg cag cag ctg agt ggc tat ttc ctg cag ctg aaa ttt		1073	
Glu Glu Tyr Val Gln Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe			
240	245	250	
gac cca gag ctg ctg ttc ggt gtc cag ttc caa tac cgc aac cgc att		1121	
Asp Pro Glu Leu Leu Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile			
255	260	265	
gcc atg gag ttc aac cat ctc tac cac tgg cac ccc ctc atg cct gac		1169	
Ala Met Glu Phe Asn His Leu Tyr His Trp His Pro Leu Met Pro Asp			
270	275	280	
tcc ttc aag gtg ggc tcc cag gag tac agc tac gag cag ttc ttg ttc		1217	
Ser Phe Lys Val Gly Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe			
285	290	295	
aac acc tcc atg ttg gtg gac tat ggg gtt gag gcc ctg gtg gat gcc		1265	
Asn Thr Ser Met Leu Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala			
300	305	310	315
tcc tct cgc cag att gct ggc cgg atc ggt ggg ggc agg aac atg gac		1313	
Phe Ser Arg Gln Ile Ala Gly Arg Ile Gly Gly Arg Asn Met Asp			
320	325	330	
cac cac atc ctg cat gtg gct gtg gat gtc atc agg gag tct cgg gag		1361	
His His Ile Leu His Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu			
335	340	345	
atg cggtt cgtt cttt cttt aat gag tac cgc aag agg ttt ggc atg aaa		1409	
Met Arg Leu Gln Pro Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys			
350	355	360	
ccc tac acc tcc ttc cag gag ctc gta gga gag aag gag atg gca gca		1457	
Pro Tyr Thr Ser Phe Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala			
365	370	375	
gag ttg gag gaa ttg tat gga gac att gat gcg ttg gag ttc tac cct		1505	
Glu Leu Glu Leu Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro			
380	385	390	395
gga ctg ctt ctt gaa aag tgc cat cca aac tct atc ttt ggg gag agt		1553	
Gly Leu Leu Leu Glu Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser			
400	405	410	
atg ata gag att ggg gct ccc ttt tcc ctc aag ggt ctc cta ggg aat		1601	
Met Ile Glu Ile Gly Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn			

415	420	425	
ccc atc tgt tct ccg gag tac tgg aag ccg agc aca ttt ggc ggc gag Pro Ile Cys Ser Pro Glu Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu			1649
430	435	440	
gtg ggc ttt aac att gtc aag acg gcc aca ctg aag aag ctg gtc tgc Val Gly Phe Asn Ile Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys			1697
445	450	455	
ctc aac acc aag acc tgt ccc tac gtt tcc ttc cgt gtg ccg gat gcc Leu Asn Thr Lys Thr Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala			1745
460	465	470	475
agt cag gat gat ggg cct gct gtg gag cga cca tcc aca gag Ser Gln Asp Asp Gly Pro Ala Val Glu Arg Pro Ser Thr Glu			1787
480	485		
ctctgagggg caggaaagca gcattctgga gggagagct ttgtgcttgt cattccagag			1847
tgctgaggcc agggctgatg gtcttaatg ctcatttct ggtttggcat ggtgagtgtt			1907
ggggttgaca tttagaactt taagtctcac ccattatctg gaatattgtg attctgttta			1967
ttcttccaga atgctgaact ccttgtagc cttcagatt gttaggagtg gttctcattt			2027
ggtctgccag aatactgggt tcttagtgta caacctagaa tgcagattt ctggttgatt			2087
tgtAACACAG tcattctagg atgtggagct actgatgaaa tctgctagaa agttaggggg			2147
ttcttatttt gcattccaga atcttgactt tctgatttgtt gattcaaagt gttgtgttcc			2207
tggctgatga tccagaacag tggctcgat cccaaatctg tcagcatctg gctgtctaga			2267
atgtggattt gattcatttt cctgttcaagt gagatatcat agagacggag atcctaaggt			2327
ccaacaagaa tgcattccct gaatctgtgc ctgcactgag agggcaagga agtggggtgt			2387
tcttcggg acccccacta agaccctggt ctgaggatgt agagagaaca ggtgggctgt			2447
attcacgcac ttgggtggaa gctaccagag ctctatcccc atccaggtct tgactcatgg			2507
cagctgtttc tcatgaagct aataaaattc gc			2539

<210> 20
 <211> 1875
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (232)..(519)

<400> 20
 ggccgggtgct gcgctcctct aattggact ccgagccggg gctatttctg gcgctggccg 60
 ggctccaaga aggcacccgc atttgctacc agcggcggcc gcggcggagc caggccggtc 120
 ctcagcgccc agcaccgccc ctcccggcaa cccggagcgc gcaccgcagc cggcggccga 180
 gctcgcgcat cccagccatc actcttccac ctgctcctta gagaagggaa g atg agt 237
 Met Ser
 1

gag tcg agc tcg aag tcc agc cag ccc ttg gcc tcc aag cag gaa aag 285
 Glu Ser Ser Ser Lys Ser Ser Gln Pro Leu Ala Ser Lys Gln Glu Lys
 5 10 15

gac ggc act gag aag cgg ggc cgg ggc agg ccg cgc aag cag cct ccg 333
 Asp Gly Thr Glu Lys Arg Gly Arg Gly Arg Pro Arg Lys Gln Pro Pro
 20 25 30

aag gag ccc agc gaa gtg cca aca cct aag aga cct cgg ggc cga cca 381
 Lys Glu Pro Ser Glu Val Pro Thr Pro Lys Arg Pro Arg Gly Arg Pro
 35 40 45 50

aag gga agc aaa aac aag ggt gct gcc aag acc cgg aaa acc acc aca 429
 Lys Gly Ser Lys Asn Lys Gly Ala Ala Lys Thr Arg Lys Thr Thr Thr
 55 60 65

act cca gga agg aaa cca agg ggc aga ccc aaa aaa ctg gag aag gag 477
 Thr Pro Gly Arg Lys Pro Arg Gly Arg Pro Lys Lys Leu Glu Lys Glu
 70 75 80

gaa gag gag ggc atc tcg cag gag tcc tcg gag gag gag cag 519
 Glu Glu Glu Gly Ile Ser Gln Glu Ser Ser Glu Glu Glu Gln
 85 90 95

tgaccatgc gtgccgcctg ctcctcactg gaggagcagc ttccctctgg gactggacag 579
 ctggctccg ctccccccgc ccccgccct tccccaggcc caccatcacc accgcctctg 639
 gccgccaccc ccatcttcca cctgtgcctt caccaccaca ctacacagca caccagccgc 699
 tgcagggctc ccatgggctg agtggggagc agttttcccc tggcctcagt tcccagctcc 759
 ccccgcccac ccacgcatac acacatgccc tcctggacaa ggctaacatc ccacttagcc 819
 gcaccctgca cctgctgcgt ccccaactccc ttgggtggtgg ggacattgct ctctgggctt 879
 ttggtttggg ggcgcctct ctgcctcctt cactgttccc tctggcttcc catagtgggg 939
 cctgggaggg ttccccctgg ccttaaaagg ggcccaagcc catctcatcc tggcacgccc 999
 tactccactg ccctggcagc agcaggtgtg gccaatggag gggggtgctg gccccccagga 1059

ttcccccagc caaactgtct ttgtcaccac gtggggctca ctttcatcc ttcccccaact 1119
 tccctagtcc ccgtactagg ttggacagcc cccttcggct acaggaaggc aggaggggtg 1179
 agtcccctac tccctttca ctgtggccac agcccccttg ccctccgcct gggatctgag 1239
 tacatattgt ggtgatggag atgcagtcac ttattgtcca ggtgaggccc aagagccctg 1299
 tggccgccac ctgaggtggg ctggggctgc tcccttaacc ctactttgct tccgccactc 1359
 agccatttcc ccctcctcag atggggcacc aataacaagg agtcacccct gcccgtccc 1419
 aaccccccctc ctgctcctcc ctgccccca aggttctggt tccattttc ctctgttcac 1479
 aaactacctc tggacagttg tggtgtttt tggtcaatgt tccattttc gacatccgtc 1539
 attgctgctg ctaccagcgc caaatgtca tcctcattgc ctccctgtct gcccacgatc 1599
 ccctccccca agatactctt tgtgggaaag aggggctggg gcatggcagg ctgggtgacc 1659
 gactacccca gtcccaggga aggtgcctg cccctaggat gctgcagcag agtgagcaag 1719
 ggggccccgaa tcgaccataa agggtgttagg ggccacctcc tccccctgtt ctgttgggaa 1779
 ggggtagcca tgatttgc cagcctgggg ctccctctct ggttccatat ttacagttac 1839
 ttgaataaaa aaaatatcct tttctggaaa aaaaaa 1875

<210> 21
 <211> 626
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (96)..(332)

<400> 21
 agtctccggc gagttgtgc ctgggctgga cgtggtttg tctgctgcgc ccgctttcg 60
 cgctctcggt tcattttctg cagcgcgccca cgagg atg gcc cac aag cag atc 113
 Met Ala His Lys Gln Ile
 1 5

tac tac tcg gac aag tac ttc gac gaa cac tac gag tac cgg cat gtt 161
 Tyr Tyr Ser Asp Lys Tyr Phe Asp Glu His Tyr Glu Arg His Val
 10 15 20

atg tta ccc aga gaa ctt tcc aaa caa gta cct aaa act cat ctg atg 209
 Met Leu Pro Arg Glu Leu Ser Lys Gln Val Pro Lys Thr His Leu Met
 25 30 35

tct gaa gag gag tgg agg aga ctt ggt gtc caa cag agt cta ggc tgg 257
 Ser Glu Glu Glu Trp Arg Arg Leu Gly Val Gln Gln Ser Leu Gly Trp
 40 45 50

gtt cat tac atg att cat gag cca gaa cca cat att ctt ctc ttt aga 305
 Val His Tyr Met Ile His Glu Pro Glu Pro His Ile Leu Leu Phe Arg
 55 60 65 70

cga cct ctt cca aaa gat caa caa aaa tgaagtttat ctggggatcg 352
 Arg Pro Leu Pro Lys Asp Gln Gln Lys
 75

tcaaatcttt ttcaaattta atgtatatgt gtatataagg tagtattcag tgaatacttg 412
 agaaaatgtac aaatcttca tccataacctg tgcatgagct gtattcttca cagcaacaga 472
 gctcagttaa atgcaactgc aagtaggtta ctgtaagatg tttaagataa aagttcttcc 532
 agtcagttt tctcttaagt gcctgttga gtttactgaa acagtttact tttgttcaat 592
 aaagtttgcattt tttttttttt aaaaaaaaaaaaaaaa aaaaa 626

<210> 22
<211> 3480
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (268) .. (2922)

<400> 22
ggcggagatc gcgtctcttt cgctccgtgt ccgcgtgtgc tcctgtgagc gccccggcgag 60
tccgtcccgt ccaccgtccg cagctggtag ccagcctgcc cctcgccctcg actccctttc 120
accaacaccg acacccacat tgacacacctc agtccggcca gccgctccac tcgttgcctt 180
tgcatctcca cacatggcgt cctcgccgag agcggcggct cctccggggg acccgccggtc 240
cccaccgtgc agcggggcat catcaag atg gtc ctc tca ggg tgc gcc atc att 294
Met Val Leu Ser Gly Cys Ala Ile Ile
1 5

gtc cga ggt cag cct cgt ggt ggg cct cct gag cgg cag atc aac 342
Val Arg Gly Gln Pro Arg Gly Gly Pro Pro Pro Glu Arg Gln Ile Asn
10 15 20 25

ctc agc aac att cgt gct gga aat ctt gct cgc cgg gca gcc gcc aca 390
Leu Ser Asn Ile Arg Ala Gly Asn Leu Ala Arg Arg Ala Ala Ala Thr
30 35 40

caa cct gat gca aag gat acc cct gat gag ccc tgg gca ttt cca gct	438
Gln Pro Asp Ala Lys Asp Thr Pro Asp Glu Pro Trp Ala Phe Pro Ala	
45 50 55	
cga gag ttc ctt cga aag aag ctg att ggg aag gaa gtc tgt ttc acg	486
Arg Glu Phe Leu Arg Lys Lys Leu Ile Gly Lys Glu Val Cys Phe Thr	
60 65 70	
ata gaa aac aag act ccc cag ggg cga gag tat ggc atg atc tac ctt	534
Ile Glu Asn Lys Thr Pro Gln Gly Arg Glu Tyr Gly Met Ile Tyr Leu	
75 80 85	
gga aaa gat acc aat ggg gaa aac att gca gaa tca ctg gtt gca gag	582
Gly Lys Asp Thr Asn Gly Glu Asn Ile Ala Glu Ser Leu Val Ala Glu	
90 95 100 105	
ggc tta gcc acc cgg aga gaa ggc atg aga gct aat aat cct gag cag	630
Gly Leu Ala Thr Arg Arg Glu Gly Met Arg Ala Asn Asn Pro Glu Gln	
110 115 120	
aac cgg ctt tca gaa tgt gaa gaa caa gca aag gca gcc aag aaa ggg	678
Asn Arg Leu Ser Glu Cys Glu Glu Gln Ala Lys Ala Ala Lys Lys Gly	
125 130 135	
atg tgg agt gag ggg aac ggt tca cat act atc cgg gat ctc aag tat	726
Met Trp Ser Glu Gly Asn Gly Ser His Thr Ile Arg Asp Leu Lys Tyr	
140 145 150	
acc att gaa aac cca agg cac ttt gtg gac tca cac cac cag aag cct	774
Thr Ile Glu Asn Pro Arg His Phe Val Asp Ser His His Gln Lys Pro	
155 160 165	
gtt aat gct atc atc gag cat gtg cgg gac ggc agt gtg gtc agg gcc	822
Val Asn Ala Ile Ile Glu His Val Arg Asp Gly Ser Val Val Arg Ala	
170 175 180 185	
ctg ctc ctc cca gat tac tac ctg gtt aca gtc atg ctg tca ggc atc	870
Leu Leu Leu Pro Asp Tyr Tyr Leu Val Thr Val Met Leu Ser Gly Ile	
190 195 200	
aag tgc cca act ttt cga cgg gaa gca gat ggc agt gaa act cca gag	918
Lys Cys Pro Thr Phe Arg Arg Glu Ala Asp Gly Ser Glu Thr Pro Glu	
205 210 215	
cct ttt gct gca gaa gcc aaa ttt ttc act gag tcg cga ctg ctt cag	966
Pro Phe Ala Ala Glu Ala Lys Phe Phe Thr Glu Ser Arg Leu Leu Gln	
220 225 230	
aga gat gtt cag atc att ctg gag agc tgc cac aac cag aac att gtg	1014
Arg Asp Val Gln Ile Ile Leu Glu Ser Cys His Asn Gln Asn Ile Val	
235 240 245	
ggt acc atc ctt cat cca aat ggc aac atc aca gag ctc ctc ctg aag	1062
Gly Thr Ile Leu His Pro Asn Gly Asn Ile Thr Glu Leu Leu Lys	

250	255	260	265	
gaa ggt ttc gca cgc tgt gtg gac tgg tcg att gca gtt tac acc cgg Glu Gly Phe Ala Arg Cys Val Asp Trp Ser Ile Ala Val Tyr Thr Arg 270		275	280	1110
ggc gca gaa aag ctg agg gcg gca gag agg ttt gcc aaa gag cgc agg Gly Ala Glu Lys Leu Arg Ala Ala Glu Arg Phe Ala Lys Glu Arg Arg 285		290	295	1158
ctg aga ata tgg aga gac tat gtg gct ccc aca gct aat ttg gac caa Leu Arg Ile Trp Arg Asp Tyr Val Ala Pro Thr Ala Asn Leu Asp Gln 300	305	310		1206
aag gac aag cag ttt gtt gcc aag gtg atg cag gtt ctg aat gct gat Lys Asp Lys Gln Phe Val Ala Lys Val Met Gln Val Leu Asn Ala Asp 315	320	325		1254
gcc att gtt gtg aag ctg aac tca ggc gat tac aag acg att cac ctg Ala Ile Val Val Lys Leu Asn Ser Gly Asp Tyr Lys Thr Ile His Leu 330	335	340	345	1302
tcc agc atc cga cca ccg agg ctg gag ggg gag aac acc cag gat aag Ser Ser Ile Arg Pro Pro Arg Leu Glu Gly Glu Asn Thr Gln Asp Lys 350	355	360		1350
aac aag aaa ctg cgt ccc ctg tat gac att cct tac atg ttt gag gcc Asn Lys Lys Leu Arg Pro Leu Tyr Asp Ile Pro Tyr Met Phe Glu Ala 365	370	375		1398
cgg gaa ttt ctt cga aaa aag ctt att ggg aag aag gtc aat gtg acg Arg Glu Phe Leu Arg Lys Lys Leu Ile Gly Lys Lys Val Asn Val Thr 380	385	390		1446
gtg gac tac att aga cca gcc agc cca gcc aca gag aca gtg cct gcc Val Asp Tyr Ile Arg Pro Ala Ser Pro Ala Thr Glu Thr Val Pro Ala 395	400	405		1494
ttt tca gag cgt acc tgt gcc act gtc acc att gga gga ata aac att Phe Ser Glu Arg Thr Cys Ala Thr Val Thr Ile Gly Gly Ile Asn Ile 410	415	420	425	1542
gct gag gct ctt gtc agc aaa ggt cta gcc aca gtg atc aga tac cgg Ala Glu Ala Leu Val Ser Lys Gly Leu Ala Thr Val Ile Arg Tyr Arg 430	435	440		1590
cag gat gat gac cag aga tca tca cac tac gat gaa ctg ctt gct gca Gln Asp Asp Asp Gln Arg Ser Ser His Tyr Asp Glu Leu Leu Ala Ala 445	450	455		1638
gag gcc aga gct att aag aat ggc aaa gga ttg cat agc aag aag gaa Glu Ala Arg Ala Ile Lys Asn Gly Lys Gly Leu His Ser Lys Lys Glu 460	465	470		1686

gtg cct atc cac cgt gtt gca gat ata tct ggg gat acc caa aaa gca Val Pro Ile His Arg Val Ala Asp Ile Ser Gly Asp Thr Gln Lys Ala 475 480 485	1734
aag cag ttc ctg cct ttt ctt cag cg ^g gca ggt cgt tct gaa gct gtg Lys Gln Phe Leu Pro Phe Leu Gln Arg Ala Gly Arg Ser Glu Ala Val 490 495 500 505	1782
gtg gaa tac gtc ttc agt ggt tct cgt ctc aaa ctc tat ttg cca aag Val Glu Tyr Val Phe Ser Gly Ser Arg Leu Lys Leu Tyr Leu Pro Lys 510 515 520	1830
gaa act tgc ctt atc acc ttc ttg ctt gca ggc att gaa tgc ccc aga Glu Thr Cys Leu Ile Thr Phe Leu Leu Ala Gly Ile Glu Cys Pro Arg 525 530 535	1878
gga gcc cga aac ctc cca ggc ttg gtg cag gaa gga gag ccc ttc agc Gly Ala Arg Asn Leu Pro Gly Leu Val Gln Glu Gly Glu Pro Phe Ser 540 545 550	1926
gag gaa gct aca ctt ttc acc aag gaa ctg gtg ctg cag cga gag gtg Glu Glu Ala Thr Leu Phe Thr Lys Glu Leu Val Leu Gln Arg Glu Val 555 560 565	1974
gag gtg gag gtg gag agc atg gac aag gcc ggc aac ttt atc ggc tgg Glu Val Glu Val Glu Ser Met Asp Lys Ala Gly Asn Phe Ile Gly Trp 570 575 580 585	2022
ctg cac atc gac ggt gcc aac ctg tcc gtc ctg ctg gtg gag cac gc ^g Leu His Ile Asp Gly Ala Asn Leu Ser Val Leu Leu Val Glu His Ala 590 595 600	2070
ctc tcc aag gtc cac ttc acc gcc gaa cgc agc tcc tac tac aag tcc Leu Ser Lys Val His Phe Thr Ala Glu Arg Ser Ser Tyr Tyr Lys Ser 605 610 615	2118
ctg ctg tct gcc gag gag gcc gca aag cag aag aaa gag aag gtc tgg Leu Leu Ser Ala Glu Glu Ala Ala Lys Gln Lys Lys Glu Lys Val Trp 620 625 630	2166
gcc cac tat gag gag cag ccc gtg gag gag gtg atg cca gtg ctg gag Ala His Tyr Glu Glu Gln Pro Val Glu Glu Val Met Pro Val Leu Glu 635 640 645	2214
gag aag gag cga tct gct agc tac aag ccc gtg ttt gtg acc gag atc Glu Lys Glu Arg Ser Ala Ser Tyr Lys Pro Val Phe Val Thr Glu Ile 650 655 660 665	2262
act gat gac ctg cac ttc tac gtg cag gat gtg gag acc ggc acc cag Thr Asp Asp Leu His Phe Tyr Val Gln Asp Val Glu Thr Gly Thr Gln 670 675 680	2310
ttc cag aag ctg atg gag aac atg cgc aat gac att gcc agt cac ccc Phe Gln Lys Leu Met Glu Asn Met Arg Asn Asp Ile Ala Ser His Pro	2358

685	690	695	
cct gta gag ggc tcc tat gcc ccc cgc agg gga gag ttc tgc att gcc Pro Val Glu Gly Ser Tyr Ala Pro Arg Arg Gly Glu Phe Cys Ile Ala			2406
700 705 710			
aaa ttt gta gat gga gaa tgg tac cgt gcc cga gta gag aaa gtc gag Lys Phe Val Asp Gly Glu Trp Tyr Arg Ala Arg Val Glu Lys Val Glu			2454
715 720 725			
tct cct gcc aaa ata cat gtc ttc tac att gac tac ggc aac aga gag Ser Pro Ala Lys Ile His Val Phe Tyr Ile Asp Tyr Gly Asn Arg Glu			2502
730 735 740 745			
gtc ctg cca tcc acc cgc ctg ggt acc cta tca cct gcc ttc agc act Val Leu Pro Ser Thr Arg Leu Gly Thr Leu Ser Pro Ala Phe Ser Thr			2550
750 755 760			
cgg gtg ctg cca gct caa gcc acg gag tat gcc ttc gcc ttc atc cag Arg Val Leu Pro Ala Gln Ala Thr Glu Tyr Ala Phe Ala Phe Ile Gln			2598
765 770 775			
gtg ccc caa gat gat gat gcc cgc acg gac gcc gtg gac agc gta gtt Val Pro Gln Asp Asp Asp Ala Arg Thr Asp Ala Val Asp Ser Val Val			2646
780 785 790			
cgg gat atc cag aac act cag tgc ctg ctc aac gtg gaa cac ctg agt Arg Asp Ile Gln Asn Thr Gln Cys Leu Leu Asn Val Glu His Leu Ser			2694
795 800 805			
gcc ggc tgc ccc cat gtc acc ctg cag ttt gca gat tcc aag ggc gat Ala Gly Cys Pro His Val Thr Leu Gln Phe Ala Asp Ser Lys Gly Asp			2742
810 815 820 825			
gtg ggg ctg ggc ttg gtg aag gaa ggg ctg gtc atg gtg gag gtg cgc Val Gly Leu Gly Leu Val Lys Glu Gly Leu Val Met Val Glu Val Arg			2790
830 835 840			
aag gag aaa cag ttc cag aaa gtg atc aca gaa tac ctg aat gcc caa Lys Glu Lys Gln Phe Gln Lys Val Ile Thr Glu Tyr Leu Asn Ala Gln			2838
845 850 855			
gag tca gcc aag agc gcc agg ctg aac ctg tgg cgc tat gga gac ttt Glu Ser Ala Lys Ser Ala Arg Leu Asn Leu Trp Arg Tyr Gly Asp Phe			2886
860 865 870			
cga gct gat gat gca gac gaa ttt ggc tac agc cgc taaggagggg Arg Ala Asp Asp Ala Asp Glu Phe Gly Tyr Ser Arg			2932
875 880 885			
atcggtttg gccccagcc cccgtcacgc cagtccctct tcctctgccg ggagggttt 2992			
ttcaactcca aaccccagag aggggttgta cattgggtcc agctttgctt cagtgtgtgg 3052			

aaatgtctcg tggggtggca tcggggctgc ggggtgggga ccccaaggct ttctgggca 3112
 gacccttgc ctctggatg atggcactg ctatccacag tctctgccag ttggtttat 3172
 ttggaggttt gtgggctttt taaaaaaaaaaa aaaagtccctc aaatcaggaa gaaacatcaa 3232
 agactatgtc ctagtgagg gagtaatcct aacacccagg ctggccgcca gctggcacct 3292
 gcctctatcc cagactgccc tcgtcccagc tctctgtcca actgttgatt atgtgatttt 3352
 tctgatacgt ccattctcaa atgccagtgt gttcacatct tcgctctggc cagcccattc 3412
 tgtatttaaa gcttttgag gcccaataaaa atagtacgtg ctgctgcagc ccttattgat 3472
 caaaaaaaaaa 3480

<210> 23
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 23
 Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
 1 5 10 15

Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
 20 25 30

Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
 35 40 45

Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
 50 55 60

Glu Ile Met
 65

<210> 24
 <211> 604
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
 1 5 10 15

Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
 20 25 30

Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly

35	40	45
Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys		
50	55	60
Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His		
65	70	75
80		
Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn		
85	90	95
Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser		
100	105	110
Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe		
115	120	125
Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp		
130	135	140
Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Gln Leu Pro Asp Ser		
145	150	155
160		
Asn Glu Ile Val Glu Lys Leu Leu Leu Arg Arg Lys Phe Ile Pro Asp		
165	170	175
Pro Gln Gly Ser Asn Met Met Phe Ala Phe Phe Ala Gln His Phe Thr		
180	185	190
His Gln Phe Phe Lys Thr Asp His Lys Arg Gly Pro Ala Phe Thr Asn		
195	200	205
Gly Leu Gly His Gly Val Asp Leu Asn His Ile Tyr Gly Glu Thr Leu		
210	215	220
Ala Arg Gln Arg Lys Leu Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr		
225	230	240
Gln Ile Ile Asp Gly Glu Met Tyr Pro Pro Thr Val Lys Asp Thr Gln		
245	250	255
Ala Glu Met Ile Tyr Pro Pro Gln Val Pro Glu His Leu Arg Phe Ala		
260	265	270
Val Gly Gln Glu Val Phe Gly Leu Val Pro Gly Leu Met Met Tyr Ala		
275	280	285
Thr Ile Trp Leu Arg Glu His Asn Arg Val Cys Asp Val Leu Lys Gln		
290	295	300
Glu His Pro Glu Trp Gly Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu		
305	310	320
Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Gln		

325	330	335
His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu		
340	345	350
Phe Asn Lys Gln Phe Gln Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn		
355	360	365
Thr Leu Tyr His Trp His Pro Leu Leu Pro Asp Thr Phe Gln Ile His		
370	375	380
Asp Gln Lys Tyr Asn Tyr Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu		
385	390	395
Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile		
405	410	415
Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys		
420	425	430
Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser		
435	440	445
Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe		
450	455	460
Glu Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu		
465	470	475
Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu		
485	490	495
Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly		
500	505	510
Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro		
515	520	525
Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile		
530	535	540
Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly		
545	550	555
Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr		
565	570	575
Val Thr Ile Asn Ala Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn		
580	585	590
Pro Thr Val Leu Leu Lys Glu Arg Ser Thr Glu Leu		
595	600	

<210> 25
<211> 360
<212> PRT
<213> Homo sapiens

<400> 25
Met Glu Asp Phe Asn Met Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys
1 5 10 15
Gly Glu Asp Leu Ser Asn Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe
20 25 30
Leu Leu Asp Ala Ala Pro Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys
35 40 45
Tyr Phe Val Val Ile Ile Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu
50 55 60
Gly Asn Ser Leu Val Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg
65 70 75 80
Ser Val Thr Asp Val Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu
85 90 95
Phe Ala Leu Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp
100 105 110
Ile Phe Gly Thr Phe Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val
115 120 125
Asn Phe Tyr Ser Gly Ile Leu Leu Ala Cys Ile Ser Val Asp Arg
130 135 140
Tyr Leu Ala Ile Val His Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr
145 150 155 160
Leu Val Lys Phe Ile Cys Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu
165 170 175
Ala Leu Pro Val Leu Leu Phe Arg Arg Thr Val Tyr Ser Ser Asn Val
180 185 190
Ser Pro Ala Cys Tyr Glu Asp Met Gly Asn Asn Thr Ala Asn Trp Arg
195 200 205
Met Leu Leu Arg Ile Leu Pro Gln Ser Phe Gly Phe Ile Val Pro Leu
210 215 220
Leu Ile Met Leu Phe Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys
225 230 235 240
Ala His Met Gly Gln Lys His Arg Ala Met Arg Val Ile Phe Ala Val
245 250 255

Val	Leu	Ile	Phe	Leu	Leu	Cys	Trp	Leu	Pro	Tyr	Asn	Leu	Val	Leu	Leu
260								265							270

Ala	Asp	Thr	Leu	Met	Arg	Thr	Gln	Val	Ile	Gln	Glu	Thr	Cys	Glu	Arg
275							280								285

Arg	Asn	His	Ile	Asp	Arg	Ala	Leu	Asp	Ala	Thr	Glu	Ile	Leu	Gly	Ile
290							295								300

Leu	His	Ser	Cys	Leu	Asn	Pro	Leu	Ile	Tyr	Ala	Phe	Ile	Gly	Gln	Lys
305							310				315				320

Phe	Arg	His	Gly	Leu	Leu	Lys	Ile	Leu	Ala	Ile	His	Gly	Leu	Ile	Ser
325								330							335

Lys	Asp	Ser	Leu	Pro	Lys	Asp	Ser	Arg	Pro	Ser	Phe	Val	Gly	Ser	Ser
340								345							350

Ser	Gly	His	Thr	Ser	Thr	Thr	Leu								
355							360								

<210> 26
<211> 198
<212> PRT
<213> Homo sapiens

<400> 26															
Met	Pro	Leu	Gly	Leu	Leu	Trp	Leu	Gly	Leu	Ala	Leu	Leu	Gly	Ala	Leu
1				5					10						15

His	Ala	Gln	Ala	Gln	Asp	Ser	Thr	Ser	Asp	Leu	Ile	Pro	Ala	Pro	Pro
20								25							30

Leu	Ser	Lys	Val	Pro	Leu	Gln	Gln	Asn	Phe	Gln	Asp	Asn	Gln	Phe	Gln
35								40							45

Gly	Lys	Trp	Tyr	Val	Val	Gly	Leu	Ala	Gly	Asn	Ala	Ile	Leu	Arg	Glu
50							55								60

Asp	Lys	Asp	Pro	Gln	Lys	Met	Tyr	Ala	Thr	Ile	Tyr	Glu	Leu	Lys	Glu
65							70				75				80

Asp	Lys	Ser	Tyr	Asn	Val	Thr	Ser	Val	Leu	Phe	Arg	Lys	Lys	Lys	Cys
85									90						95

Asp	Tyr	Trp	Ile	Arg	Thr	Phe	Val	Pro	Gly	Cys	Gln	Pro	Gly	Glu	Phe
100								105							110

Thr	Leu	Gly	Asn	Ile	Lys	Ser	Tyr	Pro	Gly	Leu	Thr	Ser	Tyr	Leu	Val
115								120							125

Arg Val Val Ser Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys
 130 135 140
 Lys Val Ser Gln Asn Arg Glu Tyr Phe Lys Ile Thr Leu Tyr Gly Arg
 145 150 155 160
 Thr Lys Glu Leu Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser
 165 170 175
 Lys Tyr Leu Gly Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile
 180 185 190
 Asp Gln Cys Ile Asp Gly
 195

<210> 27
 <211> 122
 <212> PRT
 <213> Homo sapiens

 <400> 27
 Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
 1 5 10 15

 Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
 20 25 30

 Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
 35 40 45

 Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
 50 55 60

 Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
 65 70 75 80

 Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
 85 90 95

 Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
 100 105 110

 Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
 115 120

<210> 28
 <211> 554
 <212> PRT
 <213> Homo sapiens

<400> 28
Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1 5 10 15

Gly Ser Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
20 25 30

Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
35 40 45

Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
50 55 60

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65 70 75 80

Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
85 90 95

Met Arg Phe Arg Asp Asn Thr Ala Asn Pro Ile Ala Ile Val Gln Leu
100 105 110

Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
115 120 125

Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
130 135 140

Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145 150 155 160

Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
165 170 175

Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
180 185 190

Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
195 200 205

Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
210 215 220

Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
225 230 235 240

Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser
245 250 255

Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
260 265 270

Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
275 280 285

Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
 290 295 300

Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
 305 310 315 320

Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Ser Met Gln Thr Glu
 325 330 335

Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
 340 345 350

Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Ala Thr Ala Leu Pro
 355 360 365

Arg Val Gly Pro Val Met Pro Thr Gly Gln Asp Trp Asn His Thr Pro
 370 375 380

Gln Lys Thr Asp His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro
 385 390 395 400

Gly Ser Pro Arg Ile Ser Ser Leu Arg Pro Gln Ala Leu Ser Asn Pro
 405 410 415

Ser Thr Leu Ser Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly
 420 425 430

Ser Val Leu Pro Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp
 435 440 445

Arg Thr Ser Pro Ala Glu Pro Glu Ala Ala Pro Ala Ser Glu Gly Ala
 450 455 460

Ala Arg Pro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly
 465 470 475 480

His Glu Arg Gln Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser
 485 490 495

Val Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val
 500 505 510

Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro
 515 520 525

Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr
 530 535 540

Gln Asp Asp Arg Gln Val Glu Leu Pro Val
 545 550

<210> 29
<211> 107
<212> PRT
<213> Homo sapiens

<400> 29
Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
1 5 10 15
Arg Val Ala Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala
20 25 30
Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
35 40 45
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
50 55 60
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
65 70 75 80
Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
85 90 95
Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
100 105

<210> 30
<211> 106
<212> PRT
<213> Homo sapiens

<400> 30
Met Ala His Ala Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
1 5 10 15
Arg Val Ala Leu Leu Leu Leu Leu Val Gly Ser Arg Arg Ala Ala
20 25 30
Gly Ala Ser Val Val Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu
35 40 45
Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Asn Val Arg Ser Pro
50 55 60
Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly
65 70 75 80
Lys Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln Lys Ile Ile
85 90 95
Glu Lys Ile Leu Asn Lys Gly Ser Thr Asn

100 105

<210> 31
 <211> 300
 <212> PRT
 <213> Homo sapiens

<400> 31		
Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala		
1	5	10 15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu		
20	25	30
Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro		
35	40	45
Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser		
50	55	60
Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp		
65	70	75 80
Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp		
85	90	95
Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser		
100	105	110
Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala		
115	120	125
Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly		
130	135	140
Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe		
145	150	155 160
Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr		
165	170	175
Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro		
180	185	190
Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys		
195	200	205
Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His		
210	215	220
Ser His Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser		
225	230	235 240

Asn Glu His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser
 245 250 255

Arg Glu Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val
 260 265 270

Val Asp Pro Lys Ser Lys Glu Asp Lys His Leu Lys Phe Arg Ile
 275 280 285

Ser His Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
 290 295 300

<210> 32

<211> 295

<212> PRT

<213> Homo sapiens

<400> 32

Met Glu His Gln Leu Leu Cys Cys Glu Val Glu Thr Ile Arg Arg Ala
 1 5 10 15

Tyr Pro Asp Ala Asn Leu Leu Asn Asp Arg Val Leu Arg Ala Met Leu
 20 25 30

Lys Ala Glu Glu Thr Cys Ala Pro Ser Val Ser Tyr Phe Lys Cys Val
 35 40 45

Gln Lys Glu Val Leu Pro Ser Met Arg Lys Ile Val Ala Thr Trp Met
 50 55 60

Leu Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu
 65 70 75 80

Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Leu Glu Pro Val Lys Lys
 85 90 95

Ser Arg Leu Gln Leu Leu Gly Ala Thr Cys Met Phe Val Ala Ser Lys
 100 105 110

Met Lys Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr
 115 120 125

Asp Gly Ser Ile Arg Pro Glu Glu Leu Leu Gln Met Glu Leu Leu Leu
 130 135 140

Val Asn Lys Leu Lys Trp Asn Leu Ala Ala Met Thr Pro His Asp Phe
 145 150 155 160

Ile Glu His Phe Leu Ser Lys Met Pro Glu Ala Glu Glu Asn Lys Gln
 165 170 175

Ile Ile Arg Lys His Ala Gln Thr Phe Val Ala Ser Cys Ala Thr Asp
 180 185 190

Val Lys Phe Ile Ser Asn Pro Pro Ser Met Val Ala Ala Gly Ser Val
 195 200 205

Val Ala Ala Val Gln Gly Leu Asn Leu Arg Ser Pro Asn Asn Phe Leu
 210 215 220

Ser Tyr Tyr Arg Leu Thr Arg Phe Leu Ser Arg Val Ile Lys Cys Asp
 225 230 235 240

Pro Asp Cys Leu Arg Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Glu
 245 250 255

Ser Ser Leu Arg Gln Ala Gln Gln Asn Met Asp Pro Lys Ala Ala Glu
 260 265 270

Glu Glu Glu Glu Glu Glu Val Asp Leu Ala Cys Thr Pro Thr
 275 280 285

Asp Val Arg Asp Val Asp Ile
 290 295

<210> 33

<211> 439

<212> PRT

<213> Homo sapiens

<400> 33

Met Pro Leu Asn Val Ser Phe Thr Asn Arg Asn Tyr Asp Leu Asp Tyr			
1	5	10	15

Asp Ser Val Gln Pro Tyr Phe Tyr Cys Asp Glu Glu Glu Asn Phe Tyr			
20	25	30	

Gln Gln Gln Gln Ser Glu Leu Gln Pro Pro Ala Pro Ser Glu Asp			
35	40	45	

Ile Trp Lys Lys Phe Glu Leu Leu Pro Thr Pro Pro Leu Ser Pro Ser			
50	55	60	

Arg Arg Ser Gly Leu Cys Ser Pro Ser Tyr Val Ala Val Thr Pro Phe			
65	70	75	80

Ser Leu Arg Gly Asp Asn Asp Gly Gly Gly Ser Phe Ser Thr Ala			
85	90	95	

Asp Gln Leu Glu Met Val Thr Glu Leu Leu Gly Gly Asp Met Val Asn			
100	105	110	

Gln Ser Phe Ile Cys Asp Pro Asp Asp Glu Thr Phe Ile Lys Asn Ile			
---	--	--	--

115	120	125
Ile Ile Gln Asp Cys Met Trp Ser Gly Phe Ser Ala Ala Ala Lys Leu		
130	135	140
Val Ser Glu Lys Leu Ala Ser Tyr Gln Ala Ala Arg Lys Asp Ser Gly		
145	150	160
Ser Pro Asn Pro Ala Arg Gly His Ser Val Cys Ser Thr Ser Ser Leu		
165	170	175
Tyr Leu Gln Asp Leu Ser Ala Ala Ser Glu Cys Ile Asp Pro Ser		
180	185	190
Val Val Phe Pro Tyr Pro Leu Asn Asp Ser Ser Ser Pro Lys Ser Cys		
195	200	205
Ala Ser Gln Asp Ser Ser Ala Phe Ser Pro Ser Ser Asp Ser Leu Leu		
210	215	220
Ser Ser Thr Glu Ser Ser Pro Gln Gly Ser Pro Glu Pro Leu Val Leu		
225	230	240
His Glu Glu Thr Pro Pro Thr Thr Ser Ser Asp Ser Glu Glu Glu Gln		
245	250	255
Glu Asp Glu Glu Glu Ile Asp Val Val Ser Val Glu Lys Arg Gln Ala		
260	265	270
Pro Gly Lys Arg Ser Glu Ser Gly Ser Pro Ser Ala Gly Gly His Ser		
275	280	285
Lys Pro Pro His Ser Pro Leu Val Leu Lys Arg Cys His Val Ser Thr		
290	295	300
His Gln His Asn Tyr Ala Ala Pro Pro Ser Thr Arg Lys Asp Tyr Pro		
305	310	320
Ala Ala Lys Arg Val Lys Leu Asp Ser Val Arg Val Leu Arg Gln Ile		
325	330	335
Ser Asn Asn Arg Lys Cys Thr Ser Pro Arg Ser Ser Asp Thr Glu Glu		
340	345	350
Asn Val Lys Arg Arg Thr His Asn Val Leu Glu Arg Gln Arg Arg Asn		
355	360	365
Glu Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp Gln Ile Pro Glu Leu		
370	375	380
Glu Asn Asn Glu Lys Ala Pro Lys Val Val Ile Leu Lys Lys Ala Thr		
385	390	400
Ala Tyr Ile Leu Ser Val Gln Ala Glu Glu Gln Lys Leu Ile Ser Glu		

405

410

415

Glu Asp Leu Leu Arg Lys Arg Arg Glu Gln Leu Lys His Lys Leu Glu
 420 425 430

Gln Leu Arg Asn Ser Cys Ala
 435

<210> 34
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn Pro Cys Gly Ser Lys
 1 5 10 15

Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser Glu Gln Leu Ser Arg
 20 25 30

Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln Glu Ala Arg Glu Arg
 35 40 45

Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala
 50 55 60

Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys Leu Tyr Leu Pro Thr
 65 70 75 80

Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Arg Arg Pro Gly
 85 90 95

Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp
 100 105 110

Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu
 115 120 125

Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln
 130 135 140

Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser
 145 150 155 160

Lys Arg Lys Pro

<210> 35
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 35
Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly
1 5 10 15

Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His
20 25 30

Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
35 40 45

Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val
50 55 60

Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg
65 70 75 80

Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala
85 90 95

Ala Glu Gly Pro Ser Asp Ile Pro Asp
100 105

<210> 36
<211> 173
<212> PRT
<213> Homo sapiens

<400> 36
Met Gly Arg Gly Arg Cys Val Gly Pro Ser Leu Gln Leu Arg Gly Gln
1 5 10 15

Glu Trp Arg Cys Ser Pro Leu Val Pro Lys Gly Gly Ala Ala Ala Ala
20 25 30

Glu Leu Gly Pro Gly Gly Glu Asn Met Val Arg Arg Phe Leu Val
35 40 45

Thr Leu Arg Ile Arg Arg Ala Cys Gly Pro Pro Arg Val Arg Val Phe
50 55 60

Val Val His Ile Pro Arg Leu Thr Gly Glu Trp Ala Ala Pro Gly Ala
65 70 75 80

Pro Ala Ala Val Ala Leu Val Leu Met Leu Leu Arg Ser Gln Arg Leu
85 90 95

Gly Gln Gln Pro Leu Pro Arg Arg Pro Gly His Asp Asp Gly Gln Arg
100 105 110

Pro Ser Gly Gly Ala Ala Ala Ala Pro Arg Arg Gly Ala Gln Leu Arg
115 120 125

Arg	Pro	Arg	His	Ser	His	Pro	Thr	Arg	Ala	Arg	Arg	Cys	Pro	Gly	Gly
130						135							140		
Leu	Pro	Gly	His	Ala	Gly	Gly	Ala	Ala	Pro	Gly	Arg	Gly	Ala	Ala	Gly
145					150					155			160		
Arg	Ala	Arg	Cys	Leu	Gly	Pro	Ser	Ala	Arg	Gly	Pro	Gly			
				165					170						

<210> 37
<211> 468
<212> PRT
<213> Homo sapiens

<400> 37															
Met	Val	Asp	Thr	Glu	Ser	Pro	Leu	Cys	Pro	Leu	Ser	Pro	Leu	Glu	Ala
1				5					10				15		
Gly	Asp	Leu	Glu	Ser	Pro	Leu	Ser	Glu	Glu	Phe	Leu	Gln	Glu	Met	Gly
				20				25				30			
Asn	Ile	Gln	Glu	Ile	Ser	Gln	Ser	Ile	Gly	Glu	Asp	Ser	Ser	Gly	Ser
				35				40				45			
Phe	Gly	Phe	Thr	Glu	Tyr	Gln	Tyr	Leu	Gly	Ser	Cys	Pro	Gly	Ser	Asp
				50				55			60				
Gly	Ser	Val	Ile	Thr	Asp	Thr	Leu	Ser	Pro	Ala	Ser	Ser	Pro	Ser	Ser
				65				70			75			80	
Val	Thr	Tyr	Pro	Val	Val	Pro	Gly	Ser	Val	Asp	Glu	Ser	Pro	Ser	Gly
				85					90				95		
Ala	Leu	Asn	Ile	Glu	Cys	Arg	Ile	Cys	Gly	Asp	Lys	Ala	Ser	Gly	Tyr
				100				105				110			
His	Tyr	Gly	Val	His	Ala	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg
				115				120				125			
Thr	Ile	Arg	Leu	Lys	Leu	Val	Tyr	Asp	Lys	Cys	Asp	Arg	Ser	Cys	Lys
				130				135			140				
Ile	Gln	Lys	Lys	Asn	Arg	Asn	Lys	Cys	Gln	Tyr	Cys	Arg	Phe	His	Lys
				145				150			155			160	
Cys	Leu	Ser	Val	Gly	Met	Ser	His	Asn	Ala	Ile	Arg	Phe	Gly	Arg	Met
				165					170			175			
Pro	Arg	Ser	Glu	Lys	Ala	Lys	Leu	Lys	Ala	Glu	Ile	Leu	Thr	Cys	Glu
				180				185				190			

His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys
 195 200 205
 Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys
 210 215 220
 Ala Arg Val Ile Leu Ser Gly Lys Ala Ser Asn Asn Pro Pro Phe Val
 225 230 235 240
 Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala
 245 250 255
 Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val Arg Ile
 260 265 270
 Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr
 275 280 285
 Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp
 290 295 300
 Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met
 305 310 315 320
 Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn
 325 330 335
 Gly Phe Ile Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Cys
 340 345 350
 Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu
 355 360 365
 Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys
 370 375 380
 Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met
 385 390 395 400
 Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His
 405 410 415
 Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp
 420 425 430
 Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys
 435 440 445
 Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr
 450 455 460
 Arg Asp Met Tyr
 465

<210> 38
<211> 505
<212> PRT
<213> Homo sapiens

<400> 38
Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
1 5 10 15
Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
20 25 30
Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
35 40 45
Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
50 55 60
Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
65 70 75 80
Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp
85 90 95
Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
100 105 110
Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu
115 120 125
Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp
130 135 140
Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
145 150 155 160
Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
165 170 175
Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr
180 185 190
Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile
195 200 205
Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu
210 215 220
Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg
225 230 235 240
Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu

245	250	255
Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys 260	265	270
Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp 275	280	285
Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu 290	295	300
Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala 305	310	315
Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn 325	330	335
Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu 340	345	350
Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu 355	360	365
Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu 370	375	380
Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val 385	390	395
Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile 405	410	415
Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys 420	425	430
Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln 435	440	445
Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu 450	455	460
Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu 465	470	475
Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu 485	490	495
Leu Gln Glu Ile Tyr Lys Asp Leu Tyr 500	505	

<210> 39
<211> 441

<212> PRT
<213> Homo sapiens

<400> 39
Met Glu Gln Pro Gln Glu Glu Ala Pro Glu Val Arg Glu Glu Glu
1 5 10 15
Lys Glu Glu Val Ala Glu Ala Gly Ala Pro Glu Leu Asn Gly Gly
20 25 30
Pro Gln His Ala Leu Pro Ser Ser Ser Tyr Thr Asp Leu Ser Arg Ser
35 40 45
Ser Ser Pro Pro Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly
50 55 60
Ala Ser Cys Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys
65 70 75 80
Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly
85 90 95
Phe Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Glu
100 105 110
Arg Ser Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys
115 120 125
Arg Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg
130 135 140
Phe Gly Arg Met Pro Glu Ala Glu Lys Arg Lys Leu Val Ala Gly Leu
145 150 155 160
Thr Ala Asn Glu Gly Ser Gln Tyr Asn Pro Gln Val Ala Asp Leu Lys
165 170 175
Ala Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met
180 185 190
Thr Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ala Ser His Thr
195 200 205
Ala Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys
210 215 220
Gly Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Lys Glu
225 230 235 240
Ile Ser Val His Val Phe Tyr Arg Cys Gln Cys Thr Thr Val Glu Thr
245 250 255
Val Arg Glu Leu Thr Glu Phe Ala Lys Ser Ile Pro Ser Phe Ser Ser
260 265 270

Leu Phe Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu
 275 280 285

Ala Ile Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu
 290 295 300

Val Ala Asn Gly Ser Gly Phe Val Thr Arg Glu Phe Leu Arg Ser Leu
 305 310 315 320

Arg Lys Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val
 325 330 335

Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile
 340 345 350

Ala Ala Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro
 355 360 365

Arg Val Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His
 370 375 380

Leu Gln Ala Asn His Pro Asp Ala Gln Tyr Leu Phe Pro Lys Leu Leu
 385 390 395 400

Gln Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu His Ala Gln Met
 405 410 415

Met Gln Arg Ile Lys Lys Thr Glu Thr Glu Thr Ser Leu His Pro Leu
 420 425 430

Leu Gln Glu Ile Tyr Lys Asp Met Tyr
 435 440

```

<210> 40
<211> 742
<212> PRT
<213> Homo sapiens

<400> 40
Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
   1           5           10          15
Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
   20          25          30
Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
   35          40          45
Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
   50          55          60

```

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
 65 70 75 80
 Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
 85 90 95
 Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Ser Asn Thr Ser
 100 105 110
 Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
 115 120 125
 Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
 130 135 140
 Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
 145 150 155 160
 Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
 165 170 175
 Asp Val Ser Ser Gly Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
 180 185 190
 Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
 195 200 205
 Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Thr Leu
 210 215 220
 Met Ser Thr Ser Ala Thr Ala Thr Glu Thr Ala Thr Lys Arg Gln Glu
 225 230 235 240
 Thr Trp Asp Trp Phe Ser Trp Leu Phe Leu Pro Ser Glu Ser Lys Asn
 245 250 255
 His Leu His Thr Thr Thr Gln Met Ala Gly Thr Ser Ser Asn Thr Ile
 260 265 270
 Ser Ala Gly Trp Glu Pro Asn Glu Glu Asn Glu Asp Glu Arg Asp Arg
 275 280 285
 His Leu Ser Phe Ser Gly Ser Gly Ile Asp Asp Asp Glu Asp Phe Ile
 290 295 300
 Ser Ser Thr Ile Ser Thr Thr Pro Arg Ala Phe Asp His Thr Lys Gln
 305 310 315 320
 Asn Gln Asp Trp Thr Gln Trp Asn Pro Ser His Ser Asn Pro Glu Val
 325 330 335
 Leu Leu Gln Thr Thr Arg Met Thr Asp Val Asp Arg Asn Gly Thr
 340 345 350

Thr Ala Tyr Glu Gly Asn Trp Asn Pro Glu Ala His Pro Pro Leu Ile
 355 360 365
 His His Glu His His Glu Glu Glu Thr Pro His Ser Thr Ser Thr
 370 375 380
 Ile Gln Ala Thr Pro Ser Ser Thr Thr Glu Glu Thr Ala Thr Gln Lys
 385 390 395 400
 Glu Gln Trp Phe Gly Asn Arg Trp His Glu Gly Tyr Arg Gln Thr Pro
 405 410 415
 Lys Glu Asp Ser His Ser Thr Thr Gly Thr Ala Ala Ala Ser Ala His
 420 425 430
 Thr Ser His Pro Met Gln Gly Arg Thr Thr Pro Ser Pro Glu Asp Ser
 435 440 445
 Ser Trp Thr Asp Phe Phe Asn Pro Ile Ser His Pro Met Gly Arg Gly
 450 455 460
 His Gln Ala Gly Arg Arg Met Asp Met Asp Ser Ser His Ser Ile Thr
 465 470 475 480
 Leu Gln Pro Thr Ala Asn Pro Asn Thr Gly Leu Val Glu Asp Leu Asp
 485 490 495
 Arg Thr Gly Pro Leu Ser Met Thr Thr Gln Gln Ser Asn Ser Gln Ser
 500 505 510
 Phe Ser Thr Ser His Glu Gly Leu Glu Asp Lys Asp His Pro Thr
 515 520 525
 Thr Ser Thr Leu Thr Ser Ser Asn Arg Asn Asp Val Thr Gly Gly Arg
 530 535 540
 Arg Asp Pro Asn His Ser Glu Gly Ser Thr Thr Leu Leu Glu Gly Tyr
 545 550 555 560
 Thr Ser His Tyr Pro His Thr Lys Glu Ser Arg Thr Phe Ile Pro Val
 565 570 575
 Thr Ser Ala Lys Thr Gly Ser Phe Gly Val Thr Ala Val Thr Val Gly
 580 585 590
 Asp Ser Asn Ser Asn Val Asn Arg Ser Leu Ser Gly Asp Gln Asp Thr
 595 600 605
 Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser Glu Ser Asp
 610 615 620
 Gly His Ser His Gly Ser Gln Glu Gly Ala Asn Thr Thr Ser Gly
 625 630 635 640

Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu Ala Ser
 645 650 655
 Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val Asn Ser
 660 665 670
 Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn Ser Gly Asn
 675 680 685
 Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly Glu Ala Ser
 690 695 700
 Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser Ser Glu Thr
 705 710 715 720
 Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu Gln Asn Val
 725 730 735
 Asp Met Lys Ile Gly Val
 740

<210> 41
 <211> 489
 <212> PRT
 <213> Homo sapiens

<400> 41
 Met Leu Met Arg Leu Val Leu Thr Val Arg Ser Asn Leu Ile Pro Ser
 1 5 10 15

Pro Pro Thr Tyr Asn Ser Ala His Asp Tyr Ile Ser Trp Glu Ser Phe
 20 25 30

Ser Asn Val Ser Tyr Tyr Thr Arg Ile Leu Pro Ser Val Pro Lys Asp
 35 40 45

Cys Pro Thr Pro Met Gly Thr Lys Gly Lys Lys Gln Leu Pro Asp Ala
 50 55 60

Gln Leu Leu Ala Arg Arg Phe Leu Leu Arg Arg Lys Phe Ile Pro Asp
 65 70 75 80

Pro Gln Gly Thr Asn Leu Met Phe Ala Phe Phe Ala Gln His Phe Thr
 85 90 95

His Gln Phe Phe Lys Thr Ser Gly Lys Met Gly Pro Gly Phe Thr Lys
 100 105 110

Ala Leu Gly His Gly Val Asp Leu Gly His Ile Tyr Gly Asp Asn Leu
 115 120 125

Glu Arg Gln Tyr Gln Leu Arg Leu Phe Lys Asp Gly Lys Leu Lys Tyr

130	135	140
Gln Val Leu Asp Gly Glu Met Tyr Pro Pro Ser Val Glu Glu Ala Pro		
145	150	155
Val Leu Met His Tyr Pro Arg Gly Ile Pro Pro Gln Ser Gln Met Ala		
165	170	175
Val Gly Gln Glu Val Phe Gly Leu Leu Pro Gly Leu Met Leu Tyr Ala		
180	185	190
Thr Leu Trp Leu Arg Glu His Asn Arg Val Cys Asp Leu Leu Lys Ala		
195	200	205
Glu His Pro Thr Trp Gly Asp Glu Gln Leu Phe Gln Thr Thr Arg Leu		
210	215	220
Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Glu Tyr Val Gln		
225	230	235
Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe Asp Pro Glu Leu Leu		
245	250	255
Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile Ala Met Glu Phe Asn		
260	265	270
His Leu Tyr His Trp His Pro Leu Met Pro Asp Ser Phe Lys Val Gly		
275	280	285
Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe Asn Thr Ser Met Leu		
290	295	300
Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala Phe Ser Arg Gln Ile		
305	310	315
Ala Gly Arg Ile Gly Gly Arg Asn Met Asp His His Ile Leu His		
325	330	335
Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu Met Arg Leu Gln Pro		
340	345	350
Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys Pro Tyr Thr Ser Phe		
355	360	365
Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala Glu Leu Glu Glu Leu		
370	375	380
Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro Gly Leu Leu Leu Glu		
385	390	395
Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser Met Ile Glu Ile Gly		
405	410	415
Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn Pro Ile Cys Ser Pro		

420	425	430
-----	-----	-----

Glu Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Asn Ile		
435	440	445

Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys Leu Asn Thr Lys Thr		
450	455	460

Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala Ser Gln Asp Asp Gly		
465	470	475

Pro Ala Val Glu Arg Pro Ser Thr Glu		
	485	

<210> 42

<211> 96

<212> PRT

<213> Homo sapiens

<400> 42

Met Ser Glu Ser Ser Ser Lys Ser Ser Gln Pro Leu Ala Ser Lys Gln		
1	5	10
		15

Glu Lys Asp Gly Thr Glu Lys Arg Gly Arg Gly Arg Pro Arg Lys Gln		
20	25	30

Pro Pro Lys Glu Pro Ser Glu Val Pro Thr Pro Lys Arg Pro Arg Gly		
35	40	45

Arg Pro Lys Gly Ser Lys Asn Lys Gly Ala Ala Lys Thr Arg Lys Thr		
50	55	60

Thr Thr Thr Pro Gly Arg Lys Pro Arg Gly Arg Pro Lys Lys Leu Glu		
65	70	75
		80

Lys Glu Glu Glu Glu Gly Ile Ser Gln Glu Ser Ser Glu Glu Gln		
85	90	95

<210> 43

<211> 79

<212> PRT

<213> Homo sapiens

<400> 43

Met Ala His Lys Gln Ile Tyr Tyr Ser Asp Lys Tyr Phe Asp Glu His		
1	5	10
		15

Tyr Glu Tyr Arg His Val Met Leu Pro Arg Glu Leu Ser Lys Gln Val		
20	25	30

Pro Lys Thr His Leu Met Ser Glu Glu Glu Trp Arg Arg Leu Gly Val
 35 40 45

Gln Gln Ser Leu Gly Trp Val His Tyr Met Ile His Glu Pro Glu Pro
 50 55 60

His Ile Leu Leu Phe Arg Arg Pro Leu Pro Lys Asp Gln Gln Lys
 65 70 75

<210> 44

<211> 885

<212> PRT

<213> Homo sapiens

<400> 44

Met Val Leu Ser Gly Cys Ala Ile Ile Val Arg Gly Gln Pro Arg Gly
 1 5 10 15

Gly Pro Pro Pro Glu Arg Gln Ile Asn Leu Ser Asn Ile Arg Ala Gly
 20 25 30

Asn Leu Ala Arg Arg Ala Ala Ala Thr Gln Pro Asp Ala Lys Asp Thr
 35 40 45

Pro Asp Glu Pro Trp Ala Phe Pro Ala Arg Glu Phe Leu Arg Lys Lys
 50 55 60

Leu Ile Gly Lys Glu Val Cys Phe Thr Ile Glu Asn Lys Thr Pro Gln
 65 70 75 80

Gly Arg Glu Tyr Gly Met Ile Tyr Leu Gly Lys Asp Thr Asn Gly Glu
 85 90 95

Asn Ile Ala Glu Ser Leu Val Ala Glu Gly Leu Ala Thr Arg Arg Glu
 100 105 110

Gly Met Arg Ala Asn Asn Pro Glu Gln Asn Arg Leu Ser Glu Cys Glu
 115 120 125

Glu Gln Ala Lys Ala Ala Lys Lys Gly Met Trp Ser Glu Gly Asn Gly
 130 135 140

Ser His Thr Ile Arg Asp Leu Lys Tyr Thr Ile Glu Asn Pro Arg His
 145 150 155 160

Phe Val Asp Ser His His Gln Lys Pro Val Asn Ala Ile Ile Glu His
 165 170 175

Val Arg Asp Gly Ser Val Val Arg Ala Leu Leu Leu Pro Asp Tyr Tyr
 180 185 190

Leu Val Thr Val Met Leu Ser Gly Ile Lys Cys Pro Thr Phe Arg Arg

195	200	205
Glu Ala Asp Gly Ser Glu Thr Pro Glu Pro Phe Ala Ala Glu Ala Lys		
210	215	220
Phe Phe Thr Glu Ser Arg Leu Leu Gln Arg Asp Val Gln Ile Ile Leu		
225	230	235
Glu Ser Cys His Asn Gln Asn Ile Val Gly Thr Ile Leu His Pro Asn		
245	250	255
Gly Asn Ile Thr Glu Leu Leu Lys Glu Gly Phe Ala Arg Cys Val		
260	265	270
Asp Trp Ser Ile Ala Val Tyr Thr Arg Gly Ala Glu Lys Leu Arg Ala		
275	280	285
Ala Glu Arg Phe Ala Lys Glu Arg Arg Leu Arg Ile Trp Arg Asp Tyr		
290	295	300
Val Ala Pro Thr Ala Asn Leu Asp Gln Lys Asp Lys Gln Phe Val Ala		
305	310	315
Lys Val Met Gln Val Leu Asn Ala Asp Ala Ile Val Val Lys Leu Asn		
325	330	335
Ser Gly Asp Tyr Lys Thr Ile His Leu Ser Ser Ile Arg Pro Pro Arg		
340	345	350
Leu Glu Gly Glu Asn Thr Gln Asp Lys Asn Lys Lys Leu Arg Pro Leu		
355	360	365
Tyr Asp Ile Pro Tyr Met Phe Glu Ala Arg Glu Phe Leu Arg Lys Lys		
370	375	380
Leu Ile Gly Lys Lys Val Asn Val Thr Val Asp Tyr Ile Arg Pro Ala		
385	390	395
Ser Pro Ala Thr Glu Thr Val Pro Ala Phe Ser Glu Arg Thr Cys Ala		
405	410	415
Thr Val Thr Ile Gly Gly Ile Asn Ile Ala Glu Ala Leu Val Ser Lys		
420	425	430
Gly Leu Ala Thr Val Ile Arg Tyr Arg Gln Asp Asp Asp Gln Arg Ser		
435	440	445
Ser His Tyr Asp Glu Leu Leu Ala Ala Glu Ala Arg Ala Ile Lys Asn		
450	455	460
Gly Lys Gly Leu His Ser Lys Lys Glu Val Pro Ile His Arg Val Ala		
465	470	475
Asp Ile Ser Gly Asp Thr Gln Lys Ala Lys Gln Phe Leu Pro Phe Leu		

485

490

495

Gln Arg Ala Gly Arg Ser Glu Ala Val Val Glu Tyr Val Phe Ser Gly
 500 505 510
 Ser Arg Leu Lys Leu Tyr Leu Pro Lys Glu Thr Cys Leu Ile Thr Phe
 515 520 525
 Leu Leu Ala Gly Ile Glu Cys Pro Arg Gly Ala Arg Asn Leu Pro Gly
 530 535 540
 Leu Val Gln Glu Gly Glu Pro Phe Ser Glu Glu Ala Thr Leu Phe Thr
 545 550 555 560
 Lys Glu Leu Val Leu Gln Arg Glu Val Glu Val Glu Val Glu Ser Met
 565 570 575
 Asp Lys Ala Gly Asn Phe Ile Gly Trp Leu His Ile Asp Gly Ala Asn
 580 585 590
 Leu Ser Val Leu Leu Val Glu His Ala Leu Ser Lys Val His Phe Thr
 595 600 605
 Ala Glu Arg Ser Ser Tyr Tyr Lys Ser Leu Leu Ser Ala Glu Glu Ala
 610 615 620
 Ala Lys Gln Lys Lys Glu Lys Val Trp Ala His Tyr Glu Glu Gln Pro
 625 630 635 640
 Val Glu Glu Val Met Pro Val Leu Glu Glu Lys Glu Arg Ser Ala Ser
 645 650 655
 Tyr Lys Pro Val Phe Val Thr Glu Ile Thr Asp Asp Leu His Phe Tyr
 660 665 670
 Val Gln Asp Val Glu Thr Gly Thr Gln Phe Gln Lys Leu Met Glu Asn
 675 680 685
 Met Arg Asn Asp Ile Ala Ser His Pro Pro Val Glu Gly Ser Tyr Ala
 690 695 700
 Pro Arg Arg Gly Glu Phe Cys Ile Ala Lys Phe Val Asp Gly Glu Trp
 705 710 715 720
 Tyr Arg Ala Arg Val Glu Lys Val Glu Ser Pro Ala Lys Ile His Val
 725 730 735
 Phe Tyr Ile Asp Tyr Gly Asn Arg Glu Val Leu Pro Ser Thr Arg Leu
 740 745 750
 Gly Thr Leu Ser Pro Ala Phe Ser Thr Arg Val Leu Pro Ala Gln Ala
 755 760 765
 Thr Glu Tyr Ala Phe Ala Phe Ile Gln Val Pro Gln Asp Asp Ala

770	775	780
Arg Thr Asp Ala Val Asp Ser Val Val Arg Asp Ile Gln Asn Thr Gln		
785	790	795
Cys Leu Leu Asn Val Glu His Leu Ser Ala Gly Cys Pro His Val Thr		
805	810	815
Leu Gln Phe Ala Asp Ser Lys Gly Asp Val Gly Leu Gly Leu Val Lys		
820	825	830
Glu Gly Leu Val Met Val Glu Val Arg Lys Glu Lys Gln Phe Gln Lys		
835	840	845
Val Ile Thr Glu Tyr Leu Asn Ala Gln Glu Ser Ala Lys Ser Ala Arg		
850	855	860
Leu Asn Leu Trp Arg Tyr Gly Asp Phe Arg Ala Asp Asp Ala Asp Glu		
865	870	875
Phe Gly Tyr Ser Arg		
885		

<210> 45
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 45
 agatattgca cgggagaata tacaaa

26

<210> 46
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

 <400> 46
 tcaattcctg aaatcaaagt tcggata

27

<210> 47

```

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 47
tctgcagagt tggaaggact cta          23

<210> 48
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 48
gccgaggctt ttctaccaga a          21

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 49
catggcttga tcagcaagga          20

<210> 50
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 50
tggaagtgtg ccctgaagaa g          21

```

<210> 51
<211> 23
<212> DNA
<213> Homo sapiens

<400> 51
caaggagctg acttcggAAC taa

23

<210> 52
<211> 22
<212> DNA
<213> Homo sapiens

<400> 52
aggGAAGACG ATGTGGTTT CA

22

<210> 53
<211> 22
<212> DNA
<213> Homo sapiens

<400> 53
gggACATGTG GAGAGCCTAC TC

22

<210> 54
<211> 21
<212> DNA
<213> Homo sapiens

<400> 54
catCATAGTT CCCCCGAGCA T

21

<210> 55
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 55
aAGCAGCACCC AGCAAGTGAA G

21

```

<210> 56
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 56
      tcatggcctg tgtcagtcaa a

```

21

```

<210> 57
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 57
      acatgccagc cactgtgata ga

```

22

```

<210> 58
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 58
      ccctgccttc acaatgatct c

```

21

```

<210> 59
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 59
      ggaattcacc tcaagaacat cca

```

23

<210> 60
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 60
 agtgtggcta tgacttcggt ttg

23

<210> 61
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 61
 cagccacaag cagtccagat ta

22

<210> 62
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 62
 cctgactatac aatcacatcg gaat

24

<210> 63
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 63 ccaggtgctc cacatgacag t	21
<210> 64 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic primer	
<400> 64 aaacaaccaa caacaaggag aatg	24
<210> 65 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic primer	
<400> 65 cgctctccacaca catcagcaca a	21
<210> 66 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic primer	
<400> 66 tcttggcagc aggatagtcc tt	22
<210> 67 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	

```

primer

<400> 67
gcagaccaggc atgacagatt tc          22

<210> 68
<211> 20
<212> DNA
<213> Artificial Sequence           ,
      <220>
      <223> Description of Artificial Sequence: Synthetic
            primer

<400> 68
gcggattagg gcttcctctt          20

<210> 69
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 69
ggcaccagag gcagtaacca t          21

<210> 70
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 70
agcctctctg gttctttcaa tcg         23

<210> 71
<211> 19
<212> DNA
<213> Artificial Sequence

```

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 71
tggttcacat cccgcggct

19

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 72
tggctcctca gtagcatcag

20

<210> 73
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 73
tgaagttcaa tgcactggaa ctg

23

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 74
caggacgatc tccacagcaa

20

<210> 75
<211> 23
<212> DNA

<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic primer	
<400> 75	23
tggagtccac gagatcattt aca	
<210> 76	
<211> 19	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic primer	
<400> 76	19
agccttggcc ctcggatat	
<210> 77	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic primer	
<400> 77	21
cactgagttc gccaagagca t	
<210> 78	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic primer	
<400> 78	23
cacgccatac ttgagaaggg taa	
<210> 79	
<211> 23	
<212> DNA	

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 79
gcttagtgatc aacagtggca atg 23

<210> 80

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 80
gctggcctct ccgttgag 18

<210> 81

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 81
tgttcggtgt ccagttccaa ta 22

<210> 82

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 82
tgccagtggt agagatggtt ga 22

<210> 83

<211> 22

<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
primer		
<400> 83		
acaactccag gaaggaaacc aa		22
<210> 84		
<211> 19		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
primer		
<400> 84		
cgaggactcc tgcgagatg		19
<210> 85		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
primer		
<400> 85		
tgaagaggag tggaggagac ttg		23
<210> 86		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
primer		
<400> 86		
gaatatgtgg ttctggctca tgaa		24

<210> 87
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 87
gagaaggagc gatctgctag ct 22

<210> 88
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 88
cacgtagaag tgcaggtcat cag 23